

W P E H (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat Oct 11 01:39:46 1997; MasPar time 5313.25 Seconds
Tabular output not generated. 1346.271 Million cell updates/sec
Title: >US-08-554-424-7
Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTACGCTTGGCGCATAG.....ACGGAGTATTAGTCTAGA 6513
Comp: AGATCTGCAACGGCGTATC.....TGGCTCATATCGAGATCT

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 362067 seqs, 549138275 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: emb1-new3
1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV
9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
17:VIR
Database: genbank99
18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7
25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2
31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3
38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10
45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3
52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG
59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7
66:PLN8 67:PLN9 68:PLN10 69:PLN11 70:PLN12
71:PLN13 72:PLN14 73:PLN15 74:PLN16 75:PLN17 76:PLN18 77:PLN19
78:PLN20 79:PLN21 80:PLN22 81:PLN23 82:PLN24 83:PLN25 84:PLN26
85:PLN27 86:PLN28 87:PLN29 88:PLN30 89:PLN31 90:PLN32 91:PLN33
92:PLN34 93:PLN35 94:PLN36 95:PLN37 96:PLN38 97:PLN39 98:PLN40
99:PLN41 100:PLN42 101:PLN43 102:PLN44 103:PLN45 104:PLN46
105:PLN47
Database: genbank-new3
106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV
112:MAM 113:VRT 114:PHG 115:PLN 116:PLN1 117:PLN2
118:ROD 119:SYN 120:UNA 121:VRL
Database: u-emb150_99
122:part1
Statistics: Mean 13.008; Variance 5.798; scale 2.244
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	57	Sequence 7 from patent	0.00e+00
2	6513	100.0	6513	57	Sequence 7 from patent	0.00e+00
3	5992	92.0	6883	41	Drosophila melanogast	0.00e+00
4	3676	56.4	6318	8	Musca domestica inse	0.00e+00
5	3676	56.4	6318	111	Musca domestica inse	0.00e+00
6	3676	56.4	6318	43	Musca domestica inse	0.00e+00
7	3676	56.4	6318	43	Musca domestica inse	0.00e+00
8	3664	56.3	6315	111	Musca domestica inse	0.00e+00
9	3664	56.3	6315	111	Musca domestica inse	0.00e+00
10	3663	56.2	6315	111	Musca domestica inse	0.00e+00
11	1592	24.4	2144	42	Drosophila virilis so	0.00e+00
12	1441	22.1	5068	35	Blattella germanica p	0.00e+00
13	485	7.4	1840	40	Drosophila melanogast	0.00e+00
14	391	6.0	5616	45	Squid sodium channel	0.00e+00
15	372	5.7	5352	87	Mus musculus voltage-	0.00e+00
16	354	5.6	6822	91	Rattus norvegicus sod	2.87e-286
17	354	5.4	6826	91	Rattus norvegicus sod	8.33e-288
18	352	5.4	7545	91	Rattus norvegicus sod	6.31e-286
19	342	5.3	6328	80	Human voltage-gated s	1.56e-276
20	341	5.2	5203	80	Fugu rubripes mRNA fo	1.35e-275
21	341	5.2	7823	83	Homo sapiens skeletal	1.35e-275
22	336	5.2	8552	91	Rattus norvegicus sod	6.64e-271
23	336	5.2	8553	91	Rattus norvegicus sod	6.64e-271
24	334	5.1	6957	91	Rat brain mRNA for so	4.99e-269
25	316	4.9	6396	8	Aplysia californica s	3.63e-252
26	316	4.9	6396	111	Aplysia californica s	3.63e-252
27	320	4.9	8398	91	Rat brain mRNA for so	6.55e-256
28	320	4.9	8399	91	Rattus norvegicus sod	6.55e-256
29	320	4.9	8491	81	Human cardiac tetrodo	6.55e-256
30	312	4.8	3312	40	Drosophila melanogast	2.32e-249
31	312	4.8	3312	40	Oryctolagus cuniculus	2.00e-248
32	306	4.7	5505	47	Equus caballus skelet	8.14e-243
33	308	4.7	6371	78	H.sapiens mRNA for vo	1.10e-244
34	302	4.6	542	42	Haematobia irritans e	4.44e-239
35	298	4.6	6344	92	Rattus norvegicus sod	2.41e-235
36	296	4.5	6524	91	R. norvegicus mRNA fo	1.77e-233
37	284	4.4	6373	86	M.musculus mRNA for s	2.73e-222
38	279	4.3	4169	40	Drosophila melanogast	1.23e-217
39	268	4.1	1531	90	Mus musculus (clone 3	2.08e-207
40	270	4.1	7230	50	Electrophorus electri	2.88e-209
41	270	4.1	7230	50	Electrophorus electri	2.88e-209
42	263	4.0	828	87	Mus musculus neuronal	9.11e-203
43	256	3.9	2932	42	Drosophila virilis so	2.82e-196
44	225	3.5	4844	42	Drosophila virilis so	1.20e-187
45	223	3.4	5376	45	Squid mRNA for sodium	8.31e-166

ALIGNMENTS

RESULT	1	I33685	6513 bp	DNA	PAT	27-JAN-1997
LOCUS		Sequence 7 from patent				
DEFINITION		US 5593864				
ACCESSION		I33685				
NID		g1824476				
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unclassified.				
REFERENCE		1 (bases 1 to 6513)				
AUTHORS		Arena, J.P., Feng, G., Hall, L.M., Liu, K., Van Der Ploeg, L.H.T., Wang, P. and Warmke, J.W.				
TITLE		Process for functional expression of the para cation channel				
JOURNAL		Patent: US 5593864-A 7 14-JAN-1997;				
FEATURES		Location/Qualifiers				
source		1. 6513				
BASE COUNT		1681 a 1548 c 1702 g 1582 t				
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Db 2161 Cggagcaagctggcaagattaaacatcatgacaatcccttttcatcgagccctcagagcac 2220
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Db 2221 aaacgggtggtgatgaagaatgtagtggctgaatgacatcatcgaaacaggccgctg 2280
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Db 2281 gtcgcacaagtcgggcaagcagtcgcggtgtctcgtttactatttcccaacagagagcg 2340
QY 2281 GTCGCACAGTCGGCAAGCATCGCTGCTCCGTTTACTATTTCACACAGAGGACG 2340
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Db 3181 ccgataacgatacgaataaaaatagccgagagccttcaatcgaatttggcgatttaaaagt 3240
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RESULT 2 125433 6513 bp DNA PAT 03-SEP-1996
LOCUS Sequence 7 from patent US 5550049.
DEFINITION 125433
ACCESSION g1605303
NID
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6513)
AUTHORS Van Der Ploeg, L.H.T. and Warmke, J.W.
TITLE Process for identifying para kation channel modulators
JOURNAL Patent: US 5550049-A 7 27-AUG-1996;

FEATURES
source Location/Qualifiers
1..6513
/organism="unknown"
BASE COUNT 1681 a 1548 c 1702 g 1582 t
ORIGIN

Query Match 100.0%; Score 6513; DB 57; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 gcagttgttccgtccctttaccgcgcgaatcattgtgcaaatcgaaacacgcattgcg 120
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Db 481 cattatttccctattcatcaccaaatctcgtcaactgcatcgaatcgatgataatgc 540
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Db 601 cagctgtttaaagtgtgacgaggtttcattttatgcccgttttacgtatctctagatg 660
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Qy	4141	GCTTCAAAGTGTACTTACCAACGGGTGGTGTGCTCGATTTCTGATGTATGGGTAT	4200
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<div> <div>RESULT 3</div> <div>DROSODCHA 6883 bp mRNA INV 28-SEP-1993</div> <div>LOCUS Drosophila melanogaster para locus, sodium channel alpha subunit</div> <div>DEFINITION mRNA, complete cds</div> <div>ACCESSION M32078 M24285 M32079 M32080</div> <div>NID 9403441</div> <div>KEYWORDS alternative splicing; opa repetitive sequence; sodium channel alpha subunit.</div> <div>SOURCE D.melanogaster (strain para-hd2), cDNA to mRNA, clone ZS10.3.</div> <div>ORGANISM Drosophila melanogaster</div> <div>REFERENCE 1 Eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.</div> <div>AUTHORS 1 (bases 1 to 6883)</div> <div>TITLE Loughney, K., Kreber, R. and Ganetzky, B.</div> <div>JOURNAL Molecular analysis of the para locus, a sodium channel gene in Drosophila</div> <div>MEDLINE Cell 58, 1143-1154 (1989)</div> <div>REFERENCE 2 (sites)</div> <div>AUTHORS 89376565</div> <div>TITLE Ramaswami, M. and Tanouye, M.A.</div> <div>JOURNAL Two sodium channel genes in Drosophila: Implications for channel diversity</div> <div>MEDLINE Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082 (1989)</div> <div>REFERENCE 3 (sites)</div> <div>AUTHORS Thackeray, J. R. and Ganetzky, B.</div> <div>TITLE Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms</div> <div>JOURNAL Unpublished (1993)</div> <div>COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. 58, 1143-1154 (1989)] kindly submitted by B.Ganetzky, 25-APR-1989.</div> <div>FEATURES Location/Qualifiers</div> <div>source 1..6883</div> <div>organism="Drosophila melanogaster"</div> <div>repeat_region 1..93</div> <div>cds</div> <div>join(272..3010,3173..6667)</div> <div>gene="para"</div> <div>note="Description: paralytic; alternative exon d. All para mRNAs contain either alternative exon c (see variation) or alternative exon d at this site"</div> <div>codon_start=1</div> <div>db_xref="FlyBase:FBgn0003036"</div> <div>product="sodium channel alpha subunit"</div> <div>db_xref="PID:g403444"</div> </div>			

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CDS

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Db	1335	tgtcgtctcgaggggtttggtccgaatccgaattatgcttacaccagcttcgattcgttcg	1394
QY	1087	TGTGCTCGACGGGTGTTGGTCCGAATCCGAATTTATGGCTACACGAGCTTCGATTCTGTTCCG	1146
Db	1395	gattggcttctctccgcttccgcttgatgacacaggactctctgggaggatctgtacc	1454
QY	1147	GATGGGCTTCCTGTCCGCCCTCCGGCTGATGACACAGGACTTCTCGGAGGATCTGTACC	1206
Db	1455	agctgggtgtgcgcgcgcggaccatggacatgctgtcttcttatagtcacatcttcc	1514
QY	1207	AGCTGGTGTGGCGCGCCCGGACCATGGCAATGCTGTCTTTTAGTCATCATCTTCC	1266
Db	1515	taggttcattctatcttgtgaattgtatttggccattgttggcaatgctgtacgaat	1574
QY	1267	TAGTTTCATCTATCTGTGTGAATTTGATTTGGCAATGTGTCATGCTGTATGAGCAAT	1326
Db	1575	tgcaaaaggaaagccggaagaagaggtgcgaagaaggagggcgcatacgtgaagcggaaag	1634
QY	1327	TGCAAAAGGAAGGCCGAAGAGAGGCTGCCGAAGAGAGAGCGCATACGTGAAGCGGAAG	1386
Db	1635	aagctgcgcgcgcgaagcggccaaagctggagagcggggccaaatgcgcaggctcaggcag	1694
QY	1387	ANGTGGCGCGCCAAAGCGGCCAAGCTGGAGAGCGGGGCCAAATGCCAGGCTCAGGCAG	1446
Db	1695	cagcggatgcggctgcgcgaagaagagctgcactcattccggaatggccaaagagtcgga	1754
QY	1447	CAGCGGATGCGGCTGCCCGCGAAGAGGCTGCATCGATCCGGAATGCCAAGAGTCCGA	1506
Db	1755	cgattcttgcatcagctatgagctattgttggcgcgagaaagggcaacatcacaca	1814
QY	1507	CGTATCTTGCATCAGCTATGAGCTATTTGTTGGCGCGGAGAGGGCAACGATGACACA	1566
Db	1815	acaaagagaagtgcattcggagcgcagtgtagtcggagtcggtagcggttatac	1874
QY	1567	ACAAAGAGAAGATGTCATTCCGAGCGCTCAGGTGGAGTCGGAGTCGGGTGAGCGTTATAC	1626
Db	1875	aagacaaccagcactaccacagcacaccaagctaccaaaagttctgaagtgcacga	1934
QY	1627	AAAGACACCAGCACTACCAACACACCAAGCTACAAAGTCTGTAAGTGGAGCACA	1686
Db	1935	catcttattcttaactggttcaacgttttaacatacgcagggatcacgtagttcttccaca	1994
QY	1687	CATCCTTATCTCTTACTCTGGTTACCGTTTAAATATCCGAGGGGATCACGTAGTTCTCACA	1746
Db	1995	agtacacgatacggaaacggaagcgtggccgctttgtgtatacccggtagcgatcgttaagcct	2054
QY	1747	AGTACAGGATACGGAACGGAGCTGGCCGCTTTGTTATACCCGGTAGCGATGCTAAAGCCAT	1806
Db	2055	tggtattgtcaaatatcaggtatgcgaagcagcactggccctatggccgacgactcgaatg	2114
QY	1807	TGCTATTGTACACATATCAGGATGCCAGACGACTTGGCCCTATGCGCAGCTCGAATG	1866
Db	2115	ccgtcacccgatgtccgaagaagatggggccatcatatgctcccggtgtactatggcaatc	2174
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Db	2175	taggtcccgacactcatgataacctcgatccagtcagtcacgaatctcgataccctcacatg	2234
QY	1927	TAGGCTCCGACACTCATCTGTATACCTTCGCATCAGTCAGTCCGGAATATCGTATACCTTCACATG	1986

Db	2235	gcgatctactcggcgccatggccgctcagtgccgctcagcacaatgaccaaggagagcaaat	2294
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Db	2295	tgcgcaaccgcaacacacacacatcaatcagtgggcgccacaaatggcgggcacacactgctc	2354
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Db	2355	tggaacacaatcacagaagctcgatccgcgactcgaactcgaataatggcctggagtgacggagc	2414
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Db	2415	aagctggcgaagattaaacatcatcagaaatccttttatcagagccgctcagacacaaacgg	2474
Qy	2167	RAGCTGGCAAGATTAAACATCATGACAATCTTTTATCGAGCCGCTCCAGACACAAACGG	2226
Db	2475	tggttgatgaagaatgtagtggtcctgaatgaatcgaatcgaacagcgccgctggctggcc	2534
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Qy	2287	ACAGTCGGCAAGCGATCGCGTGCTCTCCGTTTACTATTTCCTCAACAGAGGACGATGACG	2346
Db	2595	aggatggcgccgacgttcaaaagaacaggaagcactcgaagtgcattcctcaaggcatcgatggt	2654
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Qy	2467	TCUTCGATCCCTTCGTCGAGCTCTTCATCAACGCTGTGCATTTGGTCAACACGATGTTCA	2526
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Qy	2707	TGGAACCTGGGACTCGAGGGGTGCAGGGGTCTGTCGGTATTTGGTTCCTTCGATTGCTGC	2766
Db	3015	gfgattcaaaactggccaagtctttggcccaacttaattactcattcgattatgggac	3074
Qy	2767	GTGTATTCAAACTGCCAAGCTTTGGCCACACTTAATTTACTCATTTTCGATTATGGGAC	2826
Db	3075	gcaccatggcgcttgggttaactgcacatttgtacttgtcattcatcttcactctttg	3134
Qy	2827	GCACCATGGCGCTTTGGGTAACTGACATTTGTACTTTGTACTTTGCATTTATCTTCATCTTTG	2886
Db	3135	cggatggaatggaatgcaactgttcggaagaataatcatgatcaagaagccgctttcccg	3194
Qy	2887	CGGTGATGGGAATGCNACTGTTCGGAAGAATTTATCATGATCACAAGGACCGCTTTCCCG	2946
Db	3195	atggcgacctgcggcgctbgaactcaocgactttatgcacagcttcgatcggttcc	3254
Qy	2947	ATGGCGACCTGCCGCGCTGGAACTTTCACCGACTTTATGCAACAGCTTCATGATCGTGTTC	3006
Db	3255	gggtgctctcgagaatggatcgatccatgtggagctgcattgacagcttcgatcggttcc	3314
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D	b		3315	c	g	t	a	c	c	c	t	t	c	t	t	c	t	t	g	g	c	a	c	c	y	t	g	t	e	a	t	g	g	c	a	a	t	c	t	t	g	t	g	t	a	a	c	c	t	t		3374			
Q	y		3067	C	G	T	G	C	A	T	C	C	T	T	T	C	T	T	T	G	G	C	A	C	C	G	T	G	T	C	A	T	C	G	G	C	A	A	T	C	T	T	T	G	T	G	T	A	A	C	C	T	T		3126
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Q	y		3187	A	C	G	A	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		3246						
D	b		3495	a	g	c	r	t	a	a	t	t	g	c	t	a	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t		3554					
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Q	y		3307	A	T	C	A	A	C	A	T	C	A	G	T	A	G	A	G	A	C	A	C	A	G	A	T	C	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		3366					
D	b		3613	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		3665						
Q	y		3367	A	C	A	C	G	A	C	T	G	A	G	T	G	G	C	C	A	C	A	G	A	T	C	T	C	C	C	A	G	C	T	C	C	C	A	G	C	T	C	A	A	G	A	G	G	A		3426				
D	b		3666	a	c	a	c	a	g	-	a	t	c	t	c	g	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		3720						
Q	y		3427	T	C	A	A	G	A	G	A	C	G	C	A	A	C	T	G	A	G	T	G	G	C	A	T	C	G	G	G	A	T	C	G	G	G	A	T	C	A	A	T	C	A	C	A	C		3486					
D	b		3721	a	c	t	g	a	g	t																																													

[illegible]

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 P G S D R K P L V L Q T Y O A Q O H L P Y A D S N A V I P M S E N G A I I V P A Y C I N L G S R H S S Y T S H Q
 S R I S Y T S H G D L L G M A A W A G S T M T K E S K L R S R N T R N O S I G A A T N G S S T A G G Y P D A N H
 K E Q R D Y E M G Q D Y T D E A G K I K H D N P F I E P V Q T Q T V D M K D V M V L N D I I E Q A A G R S R A S
 E R G E D D E D G P T F D I A L E Y I L K I E I F C W D C C W V L K F Q E Y S F I V F D P F V E L F T I L
 C I V V N T M F M A M D H M D N P E K V L K S G N Y F T A T A F A E A S M K L A M S P K Y Y F Q B G W N I F
 D F I I V A L S L L E G L E G V Q L S V R S F R L L R V F K L A K S W P T L N L I S I M G R T M G A L G N L T
 F V L C I I I F I F A V M G W L F G K N Y I D H K D R F D H E L P R N F T D F M H S F M I V F V L C G E W I E
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 S Q Sequence 6318 BP; 1713 A; 1341 C; 1597 G; 1667 T; 0 other;

Query Match 56.4%; Score 3676; DB 8; Length 6318;
 Best Local Similarity 84.9%; Pred. No. 0.00e+00;
 Matches 4986; Conservative 0; Mismatches 806; Indels 84; Gaps 21;

Tue Oct 14 14:18:06 1997

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Query Match	56.4%;	Score 3676;	DB 111;	Length 6318;
Best Local Similarity	84.9%;	Pred. No. 0.00e+00;		
Matches	4986;	Conservative	0;	Mismatches 806; Indels 84; Gaps 21;
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DEFINITION sodium channel mRNA, complete cds.
ACCESSION U38813
NID g1783372
KEYWORDS house fly.
SOURCE Musca domestica
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscoidea; Muscidae; Musca.
REFERENCE 1 (bases 1 to 6318)
Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.
Tight genetic linkage between the kdr insecticide resistance trait
and a voltage-sensitive sodium channel gene in the house fly
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94195766
2 (bases 1 to 6318)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Characterization of voltage-sensitive sodium channel gene coding
sequences from insecticide-susceptible and knockdown-resistant
house fly strains
Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)
96245434
3 (bases 1 to 6318)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Direct Submission
Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Street, Geneva, NY 14456, USA
4 (bases 1 to 6318)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Direct Submission
Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Street, Geneva, NY 14456, USA
REMARK Nucleotide and protein update by submitter
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CDS

Tue Oct 14 14:18:06 1997

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ORIGIN

Query Match 56.4%; Score 3676; DB 43; Length 6318;
Best Local Similarity 84.9%; Pred. No. 0.00e+00;
Matches 4986; Conservative 0; Mismatches 806; Indels 84; Gaps 21;

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Tue Oct 14 14:18:06 1997

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Db	5125	gtgggtcgtctcctgcgttttagtcaaggtgtccaaggttatccgagcgtgtgtgtcgcg	5184	AUTHORS		Williamson, M.S., Martinez-Torres, D., Hick, C.A. and Devonshire, A.L.				
QY	5229	GTGGCGCGTGTCTTCGACTGTGTGAGGGAGCCAGGCAATTCGGACATCTCTCTCGC	5288	TITLE		Identification of mutations in the housefly para-type sodium channel gene associated with knockdown resistance (kdr) to pyrethroid insecticides				
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QY	5289	TTGGCCATGTCGCTGCGCGGCCCTTGTCAACATCTGCTGCTGCTGCTGCTGCTGCTG	5348	MEDLINE		96397509				
				REFERENCE		2 (bases 1 to 6899)				
				AUTHORS		Williamson, M.S.				
				TITLE		Direct Submission				
				JOURNAL		Submitted (15-MAR-1996) M.S. Williamson, IACR-Rothamsted,				

Department of Biological & Ecological Chemistry, Harpenden, Hertfordshire, AL5 2JQ, UK	
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 U38814;
 g1842213
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 20-FEB-1997 (Rel. 51, Last updated, Version 6)
 Musca domestica insecticide-resistant strain voltage-sensitive
 sodium channel mRNA, complete cds.
 Musca domestica (house fly)
 Eukaryotes; mitochondria eukaryotes; Metazoa; Arthropoda;
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 1-6315
 MEDLINE; 94195766.
 Knipple D.C., Doyle K.E., Marsella-Herrick P.A., Soderlund D.M.;
 "tight genetic linkage between the *kar* insecticide resistance
 trait and a voltage-sensitive sodium channel gene in the house
 fly";
 Proc. Natl. Acad. Sci. U.S.A. 91:2483-2487(1994).
 [2]
 1-6315
 Ingles P.J., Adams P.M., Knipple D.C., Soderlund D.M.;
 "Characterization of voltage-sensitive sodium channel gene coding
 sequences from insecticide-susceptible and knockdown-resistant
 house fly strains";
 Insect Biochem. Mol. Biol. 26:319-326(1996).
 [3]
 1-6315
 Ingles P.J., Adams P.M., Knipple D.C., Soderlund D.M.;
 Submitted (17-OCT-1995) to the EMBL/GenBank/DBJ databases.
 Dave M. Soderlund, Entomology, New York State Agricultural
 Experiment Station, Cornell University, Castle Street, Geneva, NY
 14456, USA
 [4]
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 Ingles P.J., Adams P.M., Knipple D.C., Soderlund D.M.;
 Submitted (15-JAN-1997) to the EMBL/GenBank/DBJ databases.
 Dave M. Soderlund, Entomology, New York State Agricultural
 Experiment Station, Cornell University, Castle Street, Geneva, NY
 14456, USA
 Nucleotide and protein update by submitter
 SPRENBL; Q25440.
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Qy	1707	TCACCGTTTAACATACGCGAGGGATCAGTGTAGTTCTTCAAAAGTACAGATACGGAACGGA	1766
Db	1708	cgtggacgttttgttataccaggtagcgatgcgaagccattggtactgcaaacatatcag	1767
Qy	1767	CGTGGCCGCTTTGTATATCCCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG	1826
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QY	2412	GTGTGGGACTGTGCTGGGTTGGTTGAAATTTTCAGGAGTGGGTATCCGTCATCGCTCTC	2471
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Db	2464	atggatcatcacgacatgaatccggaaatgggagaagtgctcaaaaagtggttaactatttc	2523
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QY	2892	ATGGGAATGCAACTGTTCGGAAGAATATATCATGATCAAGAGGACCGTTTCCGGATGGC	2951
Db	2884	gaattaccggctggaaatttcaccgaacttcagcacagcttcattgattgtttccgagtg	2943
QY	2952	GACCTGCGGCGCTGGAACTTCACGACATTATGCACAGCTTCATGATCGTTCGCGGTG	3011
Db	2944	ctgtcggaagatggatccagtccatctgtgggactgcagtatatgtggcgatgcagctgt	3003
QY	3012	CTCTGCGGAATGATGATCGAGTCCATGTGGGATCGATAGTGGGGCGATGCTCTGTGC	3071
Db	3004	ataccttcttttggccacgctcgatgcggcaatttggttgttcttaacttttctta	3063
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DEFINITION	Musca domestica insecticide-resistant strain voltage-sensitive sodium channel mRNA, complete cds.	INV	19-FEB-1997
ACCESSION	U38814		
NID	g1842213		
KEYWORDS	house fly.		
SOURCE	Musca domestica		
ORGANISM	Musca domestica		
REFERENCE	1 (bases 1 to 6315)		
AUTHORS	Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.		
TITLE	Tight genetic linkage between the kdr insecticide resistance trait and a voltage-sensitive sodium channel gene in the house fly		
JOURNAL	proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)		
MEDLINE	94195766		
REFERENCE	2 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Characterization of voltage-sensitive sodium channel gene coding sequences from insecticide-susceptible and knockdown-resistant house fly strains		
JOURNAL	Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)		
MEDLINE	96245434		
REFERENCE	3 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REFERENCE	4 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REMARK	Nucleotide and protein update by submitter		
FEATURES	Location/Qualifiers		
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Tue Oct 14 14:18:06 1997

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RESULT 10
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DEFINITION Musca domestica insecticide-resistant strain voltage-sensitive
sodium channel mRNA, complete cds.
ACCESSION U38814
NID 91783374
KEYWORDS house fly.
SOURCE Musca domestica
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;
Trachata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscidae; Musca.
1 (bases 1 to 6315)
Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.
Tight genetic linkage between the kdr insecticide resistance trait
and a voltage-sensitive sodium channel gene in the house fly
Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)
94195766
2 (bases 1 to 6315)
Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Characterization of voltage-sensitive sodium channel gene coding
sequences from insecticide-susceptible and knockdown-resistant
house fly strains
96245434
3 (bases 1 to 6315)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Direct Submission
Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Street, Geneva, NY 14456, USA
4 (bases 1 to 6315)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Direct Submission
Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Street, Geneva, NY 14456, USA
Nucleotide and protein update by submitter
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AUTHORS	Thackeray,J.R. and Ganetzky,B.		
TITLE	Conserved alternative splicing patterns and splicing signals in the		
JOURNAL	Drosophila sodium channel gene para		
REFERENCE	2 (bases 1 to 2144)		
AUTHORS	Thackeray,J.R. and Ganetzky,B.		
TITLE	Developmentally regulated alternative splicing generates a complex		
JOURNAL	array of drosophila para sodium channel isoforms		
MEDLINE	J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)		
REFERENCE	3 (bases 1 to 2144)		
AUTHORS	Thackeray,J.R. and Ganetzky,B.		

[illegible]

Direct Submission
Submitted (04-MAY-1995) Justin R. Thackeray, Biology, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA

Location/Qualifiers

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QY	2997	ATCGTGTTCGGGTGCTCTCGGAGAAATGGATCGAGTCCATGTTGGGACTGCAATGACG	3056
Dd	2302	ggagactggtcctgcattcccttcttcttgcactgctgctgctgctgctgctgctgctg	2361
QY	3057	GGCGATGCTCTGCGCATTCCTTCTTGGCCACCGCTTTCATCGGCAATCTGTGGTA	3116
Dd	2362	ttgaacctcttcttgccttgcctgcagcaacttgggttccatccatctgctcagccca	2421
QY	3117	CTTAACCTTTTCTAGCTTCTGTTTGTGCAATTTTGGCTCATCTAGCTTATCAGCGCCG	3176
Dd	2422	acagctgacatgaac	2481
QY	3177	ACTGGCGATTAACGATACGAAATAAATAGCCGAGGCGCTTCATCGAATTTGCGGATTA	3236
Dd	2482	aaactgataaaacgtagcgc-gctaaacgtggcaaaaattgttgcgtgcccataaataccaa	2540
QY	3237	AGTTGGGTTAAGGTAATATTCCTGATTGTTTCAAGT-TAATAGCTAACAAATTTGACAA	3295
Dd	2541	tcagatatccgatcagacccagatgccc--atgagcgtga-cac--ggacctgacctc	2595
QY	3296	TCAATAAGTGTATCAACCATCAGGTGAGGAGACCAACCATGATCAGTTGGATTGGAGCGA	3355
Dd	2596	acagcg-gctgaaatc---ctggc-c---g---atg--ga-atcgt-gtatagag---a-	2636
QY	3356	AGAGCATGGTGACAAAGNACTGGAGCTGGGCGCACGACGAGATCCTCGCGCGGCTCAT	3415
Dd	2637	caagaagatcccaaggcgacagcagcttgaggtggcagatggagaaaggagtt	2696
QY	3416	CAAGAAAGGGGATCAAGGAGCAGACCAACTGGAGTGGCCATCGGGATCGATGGAATT	3475
Dd	2697	cacctccatgagatcttgaataaagctgaagaagcagacagctgatgataagacac	2756
QY	3476	CAGATACACGGCGACATGAAGACAAACAAAGCGGAAGAAATCCAAATATCTAATAACGC	3535
Dd	2757	gaaggtgatcgccaaattcttgaataataaagacaaatcggtatgataagaa-a-gtgtga-cta	2813
QY	3536	AACGATGATTGGCAACTAATTAACCAACCAAGCAATAGACTGGAAACACGAGCTAAACCA	3595
Dd	2814	tctacaaa--tcgg--caggacgagatatttgcacacaggttgcatttgcatttgcatt	2870
QY	3596	TAGAGGTTTCTTACAGGACGACGACACTGCCAGCATTAACATCATATGTAGTCATAA	3655
Dd	2871	aaacgttccatacaaggatgacagccataagggaagtgcagagactatgattggtgagga	2930
QY	3656	GAATCGACCATTCAGGACGAGAGCCACAAAGGCGCGGAGACGATGAGGCGGAGGA	3715
Dd	2931	aaagaagaatgcagcaagaagatctcgatcaagaagaggaaggtgaagaagatggaga	2990
QY	3716	GAAGCGCGCACCAAGAGGAGGATTTAGGCTTCGACGAGGAACCTGGACGAGGAGCGGA	3775
Dd	2991	aggtgaaggacctctgagaggagacatggtattggtgagcagcact-gaggacgtcatga	3049
QY	3776	ATGCGAGGAGGGCGCGCTCGACGGTGATATCATTT-ATTATGCACACAGCAGGATATATAC	3834
Dd	3050	tgtaagaatatccgagagattgctgctcctgactcactcactataagcgtctcccttctctg	3109
QY	3835	TCGATGATATATCCAGCTGATTGCTGCCCGATTCGCTACTATTAAGAAATTTCCGATCTAG	3894
Dd	3110	ctggagacgaagactctcctcttctggcaaggctgggcaacctcgcactgaacacctcc	3169
QY	3895	CGGTGACGATGACTCGCGCTTTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTC	3954
Dd	3170	aactcattgagaaataactttgaacgctgtgataccatcactcactcactcactcactc	3229
QY	3955	AATTAATTGAAATAAATATTTTGAACAGCTGTATCAGCTATGATTTTATAGTAGTACT	4014
Dd	3230	tcgacatggcccttgaggatgtacatctgctcctcgcacacacacacacacacacacac	3289
QY	4015	TAGCTTTGGCATTTAGAAGATGTACATCTGCCACAAAGACCCATCTGCAGGATATTTAT	4074
Dd	3290	attacatggatgactcttcactcactccttcttctcactcactcactcactcactcactc	3349
QY	4075	ACTATATGGACAGATATTTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTTGG	4134
Dd	3350	cccttgggtttcaaaaaatacttcaaaaatgcttgggtgctggtggtgatttcatcttca	3409
QY	4135	CGCTCGGCTTCAAAGTGTACTTCCACACGCGGTGGTGGTGGCTCGATTTTCGTGATGTCA	4194
Dd	3410	tggtcctcactcataaaactctgtagcacttgggtggcgctggagcattcattcagccttca	3469
QY	4195	TGGTATCGCTATCAAACTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	4254
Dd	3470	aaactatgagacactcagggcccttaggaccttgggacctatgcttagaataatgcagga	3529
QY	4255	AGACTATGCGAACGTTAAGAGCACTGAGACCACTAGCTGCTCCCTGATGTCAGGGCA	4314
Dd	3530	tgaggggtggtggtgaacgcttgggtgaagccatccccagatcttcaatgtgctcctcg	3589
QY	4315	TGAGGGTCTGCTTAAATGCGCTGATACAGCTATACCGTCCATCTTCAATGTCTATTGG	4374
Dd	3590	tggtcctcactcttctggtcactcttccatcatctggtgctggtgctggtgctggtgctg	3649
QY	4375	TGTGCTTAATATTGCGCTAATTTTGGCTAATTTTGGCTAATTTTGGCTAATTTTGGCTA	4434
Dd	3650	atcataaatgtgtggtatcccaacttccacttgcagccacgaataatcctcctgacagaa	3709
QY	4435	ATTTTAAAGTGGGAGGACATGAATGGCAGCAAGCTCAGCCAGGATCATCAACCAATCGCA	4494

D	b	3710	atgcttgcattgctgtaaaactacacatggtggagaactcgcccaatgaatttttgatcaactg	3769
Q	y	4495	ATGCCTGCGAGAGCGGAGAACTACAGCTGGTGAATTTCAGCAATGAATTCGATCATGTAG	4554
D	b	3770	gcaaaccttatctctgcctctccaagtggccaccttcaaaaggatgattcagatcaatga	3829
Q	y	4555	GTAAACGGGTATCTGTGCCCTTTCCAAAGTGGCCACCTTCANAAGGTGGATACAAATCATGA	4614
D	b	3830	atgacgctaagactctagagagctccaagaacgccaatcagggaacaaacaaacatctaca	3889
Q	y	4615	ACGATGCTATCGATTACAGAGAGGTGGACACGACCACTAATTCGTGAAACGACACTACA	4674
D	b	3890	tgtacctctactttgtgtctttatcatcttttggctcatcttttccactctcaaacctatcca	3949
Q	y	4675	TGATTTATATTTTCGTATCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTCTCA	4734
D	b	3950	ttggttgatcatcgacaacttaatgagcaaaagcaaaagcaggagggtcgcctagaga	4009
Q	y	4735	TTGGTGTATTCATTTGATAATTTTATGAGCAAAAGAAAAGCAGGTGGATTCATTAGAAA	4794
D	b	4010	tgttcagctgaagatcagaagaatactacaagtctatgaagaataaggttcgaaaaa	4069
Q	y	4795	TGTTCAATGACAGAGATCAGAAAAAGTACTAATAGTCTATGAAAAGATGGCTCTAAAA	4854
D	b	4070	aacccgttaaaagccatccccagggccaaagtggagaccgcaggccactgtgttggaaatct	4129
Q	y	4855	AACCATTTAAAGCCATTCCAAAGACCAAGGTGGCGACCACAAAGCAATAGTCTTTGAAATAG	4914
D	b	4130	gcacagacaagaatttgacatgatcatcatgttttcatcttggttttaacatgttaacaa	4189
Q	y	4915	TAACCGATAGAATAATTCGATATAAATCATATGTTATTTCATTGGTCTGAACATGTTCAACA	4974
D	b	4190	tgactctggatcactatcaacagctgaagcagcttcagcgagcttcttgattactctgaaca	4249
Q	y	4975	TGACCCTCGATCGTTACGATGCGTGGACACAGCTAAGCGCGTCTGTAGACTATCTCAATG	5034
D	b	4250	tgatcttcacgtcactcttcagttccgagtgctgatgaagatatccgcccacagatacc	4309
Q	y	5035	CGATATTTCGTAGTTATTTTCAGTTCCGAATGCTATTAAAAAATATTCGCTTTACGATATC	5094
D	b	4310	actactcaagggaacatggaaacctcttgatttgcgtagttgctcatcctcatctattgg	4369
Q	y	5095	ACTATTTTATTTAGACCATGGAATTTATTTGATGTAGTAGTGTGCATTTATPCCATCTTAG	5154
D	b	4370	gtctggctatgagtgacatcattgagaaatactttgtgcctcacactgcttcgcagtg	4429
Q	y	5155	GTCTTGTACTTACGGATATATCGAGAGTACTTCGTGTCCCGACCCCTGCTCCGAGTGG	5214
D	b	4430	tgagagtggcgaaggtgggtcgagtcgctgctggtgaaagggtctaagggtattcggga	4489
Q	y	5215	TGCGTGTGGCGAAAGTGGGCGGTGCTTCGACTGTTGAAAGGAGCCAAAGGCATTCGGA	5274
D	b	4490	cattgctgttcgccttggtgatgtcttttgcacgagcgtcttcaatatctgcctactactat	4549
Q	y	5275	CACGTCTTCCTGGGTGGCCATGTGCTGCCGGCCCTGTTCAACATCTGCCTGTCTGCTGT	5334
D	b	4550	ttttagtcagtgttatttttgccactctcggcatgctctcttcattgcacgtccgcgata	4609
Q	y	5335	TCCTGGTTCATGTTCTATCTTTGCCATTTTCGGCATGTGCTTCTCATGCACTGTGAAGAGA	5394
D	b	4610	aaggtggccttgatgacgtgtacaatttcaagacgttttgggcagtcctcatgatcctgcctc	4669
Q	y	5395	AGAGCGCATTAACGACGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTGCTCT	5454
D	b	4670	tccagatgtccacatcagctgtagtggatggtgtgtttagatggtgatcatgaatgaagagg	4729
Q	y	5455	TTCAATGTGACGCTCAGCCGGTTGGATGGTGTACTGGACGCCATATTCATATGAGGAAG	5514
D	b	4730	actgcacaacaacaaatagcgaagtggctaccgggagactgtggatcagctactctgc	4789
Q	y	5515	CATCGCATCCACCCGACGACGAAAGGCTATCCCGGCAATTTGGTTTCACGACCGCTTG	5574
D	b	4790	qcatagctttctctgctcatcactcgtcatcagttttccttatcttattaacatgtaca	4849

[illegible]

QY	4554	GGTAACGGCGTATCTGTGCGCTTTTTCCTCAAGTGGCCACCTTCAAGGCTCGATACAAATCATG	4613
Db	3880	tcctgatccactgatatacagagatatcggggacacgcctattaagaaaaattcaattctt	3939
QY	4614	AACGATGCTATCGATTCACGACGAGGTGGACACAGCACCAATTCGTGAACGACATCTAC	4673
Db	3940	atgtaccttattttgtttttatcatctctcggatcattcttccaccttgaaccttttc	3999
QY	4674	ATGTATTATATTTCGTATTCTTCATCATATTGGATCCTTTTTCACACTCAATCTGTTT	4733
Db	4000	atttgggtcattatcgtataaacttttaaccacaacaaaaagggggccggcgtgagatctttggaa	4059
QY	4734	ATTGGGTATTATCATTTGATTAATTAATGAGCAAAAGAAAAAGCAGGTGGATCATTTAGAA	4793
Db	4060	gtgtttatgacgcagcagacagaaaaaatactacaaagccatgaagaccttcaatceaaa	4119
QY	4794	ATGTTCTATGACAGAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAA	4853
Db	4120	aaaccaccaagggaattccaatgcctgggtttcaaaatcgcctgaattggatgttccattta	4179
QY	4854	AAACCATTTAAAGCCATTCCAAGACCAAGTGGCGACCAAGCAATAGTCTTTGAAATA	4913
Db	4180	acaacaaatcagaanaatttgatgttgcataatcatgcttggtatcttataatatagtacact	4239
QY	4914	GTAAACCGATAAGAAATTCGATATAATCATATTATGTATTTCATTTGGCTTGAACATGTTCCAC	4973
Db	4240	atggctatggagcattatacaatgatgagaacatttgaagactcttgaatatatacaac	4299
QY	4974	ATGACCTCGATCGTTACGATCGCTGGACACGATATACGGCGGTCTCTAGACTATCTCAAT	5033
Db	4300	atggtattcatcgggaatttttaccagagaatgctgtaagatttaattggggctacgtttt	4359
QY	5034	CGCATATTCTGATTTATTTTCAGTTCCGAAATGCTCTATTAAAAATATTCGCTTTACGATAT	5093
Db	4360	tattattttaagaacacatggaaatttttgaattttgattgttagttcttcttcaactctg	4419
QY	5094	CACATATTATTTCAGCCATTCGAAATTTATTGTATGTAGTGTGTCATTTTATTCATCTTA	5153
Db	4420	ggctatgcttgcggatatttaagcaaatatttggcttctcaacattattgcgtgta	4479
QY	5154	GGTCTGTGACTTACGCAATATTATCGAAGATGACTTCGTGTCGCCGACCCCTGCCGAGTG	5213
Db	4480	gttcgtgtcttcgctgtagggcgagtctctcgtcttggtaagtcgggtaagggtatccgc	4539
QY	5214	GTGCGTGTGCGAAAGTGGCGCTGTCTTCGACTGGTGAAGGGAGCAAGGGCATTCGG	5273
Db	4540	acattgctctttccctagcagtgcttttbaactgcactctctcaacattgagtgctcta	4599
QY	5274	ACACTGTCTTTCGCTGTGGCCATGTGCTGCGCGGCCCTGTTCAACACTCTGCCTGCTGCTG	5333
Db	4600	ttttttagtatgtttattctctatgttttgaatgctatttttttaggcgtgggatat	4659
QY	5334	TTCTGTGCTATGTTTCACTTTTCGCAATTTTCGGCATGTCTGTTCTTCATGACGATGAAGAG	5393
Db	4660	ttgcaggaatagacgacgtcttcaacttccaaacttaattcaaatgattgattctttta	4719
QY	5394	AAGAGCGGCATTAACGACGCTCAACACTTCAAGACCTTTGGCCAGAGCATGATCTGCTC	5453
Db	4720	tttcaaatgctacatcagctggatgggagtggttttagctgcaatcatcgcagagcca	4779
QY	5454	TTTTCAGATGTGACGCTCAGCCGCTTGGGATGGTGTACTGTGACGGCCATTATCAATAGAGAA	5513
Db	4780	ccgccttgtaacacagatctaaaaatatttggatcaaaaaagatacaacgaagaacttggt	4839
QY	5514	---GCATGGCATCCACC-GCAGACG-----GA-CAAAAGGCTATCCG-GGCAATGTGGT	5561
Db	4840	aactacggcatggccgttatgttttgggttagctatctagtaattagctttcttctgtga	4899
QY	5562	TCACGCGCGTTGGAAATAACGTTTCTCTCTCATACCTAGTTTATAAGCTTTTTCATAGTT	5621
Db	4900	atcaacatgtatatattgcgctcatctctagaaaaacttcagcaagccacagaagtgtcaaa	4959

[illegible]

W A R E H (TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Oct 11 05:13:53 1997; MasPar time 271.74 Seconds
Tabular output not generated. 928.963 Million cell updates/sec

Title: >US-08-554-424-7
Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTAGACGTTGGCGCATAG.....ACGGAGTATTAGCTCTAGA 6513
Comp: AGATCTGCAACGGCGTATC.....TGGCTCATATCGAGATCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 74789 seqs, 19379749 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:51:2:52 3:53 4:54 5:55 6:56 7:65 8:65 9:65 10:65 11:65 12:65 13:65 14:65 15:65 16:65 17:65 18:65 19:65 20:65 21:65 22:65 23:65 24:65 25:65 26:65 27:65 28:65 29:65 30:65 31:65 32:65 33:65 34:65 35:65 36:65 37:65 38:65 39:65 40:65 41:65 42:65 43:65 44:65 45:65

Statistics: Mean 10.180; Variance 5.454; scale 1.866

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	12	PCT-US95-1 Sequence 7, Applicatio	0.00e+00
2	6513	100.0	6513	12	PCT-US95-1 Sequence 7, Applicatio	0.00e+00
3	6513	100.0	6513	5	US-08-338- Sequence 7, Applicatio	0.00e+00
4	6513	100.0	6513	5	US-08-337- Sequence 7, Applicatio	0.00e+00
5	41	0.6	215	5	US-08-238- Sequence 5, Applicatio	1.44e-10
6	36	0.6	215	5	US-08-238- Sequence 5, Applicatio	1.63e-07
7	36	0.6	1809	12	PCT-US95-1 Sequence 1, Applicatio	1.63e-07
8	39	0.6	5904	4	US-07-745- Sequence 6, Applicatio	2.48e-09
9	37	0.6	5975	6	US-08-404- Sequence 1, Applicatio	4.09e-08
10	30	0.5	33	5	US-08-338- Sequence 1, Applicatio	4.80e-04
11	30	0.5	33	12	PCT-US95-1 Sequence 1, Applicatio	4.80e-04
12	30	0.5	33	12	PCT-US95-1 Sequence 1, Applicatio	4.80e-04
13	30	0.5	33	5	US-08-337- Sequence 1, Applicatio	4.80e-04
14	31	0.5	75	5	US-08-237- Sequence 6, Applicatio	1.32e-04
15	30	0.5	1213	5	US-08-276- Sequence 6, Applicatio	4.80e-04
16	32	0.5	2356	4	US-08-001- Sequence 1, Applicatio	3.57e-05
17	32	0.5	2356	2	US-07-794- Sequence 1, Applicatio	3.57e-05
18	32	0.5	4255	13	PCT-US96-0 Sequence 14, Applicati	3.57e-05
19	32	0.5	4835	13	PCT-US96-0 Sequence 9, Applicatio	3.57e-05

20	30	0.5	5775	10	PCT-US93-0	Sequence 29, Applicati	4.80e-04
c 21	31	0.5	8438	3	US-07-945-	Sequence 1, Applicatio	1.32e-04
c 22	29	0.4	32	12	PCT-US95-1	Sequence 6, Applicatio	1.71e-03
c 23	29	0.4	32	12	PCT-US95-1	Sequence 6, Applicatio	1.71e-03
c 24	29	0.4	32	5	US-08-337-	Sequence 6, Applicatio	1.71e-03
c 25	29	0.4	32	5	US-08-338-	Sequence 6, Applicatio	1.71e-03
c 26	29	0.4	75	5	US-08-237-	Sequence 5, Applicatio	1.71e-03
c 27	29	0.4	105	4	US-07-865-	Sequence 13, Applicati	1.71e-03
c 28	29	0.4	242	6	US-08-273-	Sequence 1, Applicatio	1.71e-03
c 29	28	0.4	519	11	PCT-US94-0	Sequence 5, Applicatio	5.98e-03
c 30	27	0.4	565	6	US-08-469-	Sequence 4, Applicatio	2.04e-02
c 31	27	0.4	886	6	US-08-469-	Sequence 1, Applicatio	2.04e-02
c 32	29	0.4	1144	5	US-08-014-	Sequence 1, Applicatio	1.71e-03
c 33	28	0.4	1203	6	US-08-363-	Sequence 29, Applicati	5.98e-03
c 34	28	0.4	1203	11	PCT-US94-1	Sequence 3, Applicatio	5.98e-03
c 35	28	0.4	1710	4	US-07-903-	Sequence 4, Applicatio	5.98e-03
c 36	28	0.4	1710	5	US-08-243-	Sequence 4, Applicatio	5.98e-03
c 37	28	0.4	1710	5	US-08-283-	Sequence 3, Applicatio	5.98e-03
c 38	28	0.4	1710	6	US-08-390-	Sequence 4, Applicatio	5.98e-03
c 39	28	0.4	1710	4	US-08-044-	Sequence 3, Applicatio	5.98e-03
c 40	28	0.4	1710	6	US-08-390-	Sequence 4, Applicatio	5.98e-03
c 41	29	0.4	2329	11	PCT-US94-0	Sequence 9, Applicatio	1.71e-03
c 42	28	0.4	2950	10	PCT-US93-0	Sequence 7, Applicatio	5.98e-03
c 43	28	0.4	2968	10	PCT-US93-0	Sequence 1, Applicatio	5.98e-03
c 44	28	0.4	5011	4	US-08-141-	Sequence 1, Applicatio	5.98e-03
c 45	29	0.4	7125	4	US-07-745-	Sequence 1, Applicatio	1.71e-03

ALIGNMENTS

RESULT 1
ID PCT-US95-14378-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 7, Application PC/TUS9514378.
CC Sequence 7, Application PC/TUS9514378
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Hall, Linda
CC APPLICANT: Feng, Gouping
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Roy D. Meredith
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/14378
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meredith, Roy D.
CC REGISTRATION NUMBER: 30,777
CC REFERENCE/DOCKET NUMBER: 19332 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-4678
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6513 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear

Tue Oct 14 14:18:09 1997

CC	MOLECULE TYPE: cDNA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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Db 2101 CCTGCTGGACACCAATCACAGCTCGATCATCGGACTACGAAATGGCCCTGGAGTGA 2160
 QY 2101 CCTGCTGGACACCAATCACAGCTCGATCATCGGACTACGAAATGGCCCTGGAGTGA 2160
 Db 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAAATCCCTTTATCGAGCCCGTCCAGAC 2220
 QY 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAAATCCCTTTATCGAGCCCGTCCAGAC 2220
 Db 2221 AAACGGTGGTGTATGAAGATGTGATGGTCTCTGAATGACATCATCGACAGCCGCTG 2280
 QY 2221 AAACGGTGGTGTATGAAGATGTGATGGTCTCTGAATGACATCATCGACAGCCGCTG 2280
 Db 2281 GTGCGCACAGTGGCGAAGCGATCGGGTGTCTCGGTGTACTATTTCCCAACAGAGGAG 2340
 QY 2281 GTGCGCACAGTGGCGAAGCGATCGGGTGTCTCGGTGTACTATTTCCCAACAGAGGAG 2340
 Db 2341 ATGACGAGGATGGCGGACGTTCAAGACAAAGCACTCGAAGTGATCCTCAAAAGCATCG 2400
 QY 2341 ATGACGAGGATGGCGGACGTTCAAGACAAAGCACTCGAAGTGATCCTCAAAAGCATCG 2400
 Db 2401 ATGTGTTTGTGTGGGACTGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2460
 QY 2401 ATGTGTTTGTGTGGGACTGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2460
 Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTTGTGGTCAACAGA 2520
 QY 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTTGTGGTCAACAGA 2520
 Db 2521 TGTTCATGCGAATGATACACAGATATGAACAGAGATGAACGCGTGTCAAGAGTG 2580
 QY 2521 TGTTCATGCGAATGATACACAGATATGAACAGAGATGAACGCGTGTCAAGAGTG 2580
 Db 2581 GCAACTATTTCACCGCCACTTTGCCATCGAGCCACCATGAAGCTAATGGCCATGA 2640
 QY 2581 GCAACTATTTCACCGCCACTTTGCCATCGAGCCACCATGAAGCTAATGGCCATGA 2640
 Db 2641 GCCCAAGTACTATTTCAGAGGCGTGAACATCTTCGACTTCATTTATCGTGGCCCTAT 2700
 QY 2641 GCCCAAGTACTATTTCAGAGGCGTGAACATCTTCGACTTCATTTATCGTGGCCCTAT 2700
 Db 2701 CGCTATGGAATGGACTCGAGGCTGTCCAGGCTGTGCTCGATTTGCGTTCCTTTGAT 2760
 QY 2701 CGCTATGGAATGGACTCGAGGCTGTCCAGGCTGTGCTCGATTTGCGTTCCTTTGAT 2760
 Db 2761 TCGTGGTGTATTCAACTGGCCAAAGTCTTGCCCAACACTTAAATTTACTCATTTGATTA 2820
 QY 2761 TCGTGGTGTATTCAACTGGCCAAAGTCTTGCCCAACACTTAAATTTACTCATTTGATTA 2820
 Db 2821 TGGGACGCAACCATGGGCGCTTTGGGTAATCTGACATTTTGTACTTTGCAATTCATCTCA 2880
 QY 2821 TGGGACGCAACCATGGGCGCTTTGGGTAATCTGACATTTTGTACTTTGCAATTCATCTCA 2880
 Db 2881 TCTTTGCGGTGATGGGAATGCAACTGTTCGGAAAGAAATTAATCATGATCAAGAGCCGCT 2940
 QY 2881 TCTTTGCGGTGATGGGAATGCAACTGTTCGGAAAGAAATTAATCATGATCAAGAGCCGCT 2940
 Db 2941 TTCCGATGGCACTGGCCGCTGGAATTTACCGGACCTTTATGACAGCTTCATGATCG 3000
 QY 2941 TTCCGATGGCACTGGCCGCTGGAATTTACCGGACCTTTATGACAGCTTCATGATCG 3000
 Db 3001 TGTTCGGGTGTCTCGGAGAAATGATCGAGTCCATGTGGGACTGCAATGTACGTGGGG 3060
 QY 3001 TGTTCGGGTGTCTCGGAGAAATGATCGAGTCCATGTGGGACTGCAATGTACGTGGGG 3060
 Db 3061 ATGCTCGTGATTCCTTCTTTGGCCACCGTGTGATCGGCAATCTGTGGTACTTA 3120
 QY 3061 ATGCTCGTGATTCCTTCTTTGGCCACCGTGTGATCGGCAATCTGTGGTACTTA 3120
 Db 3121 ACCTTTCTAGCTTGTCTTGTCCAAATTTGGCTCATCTAGCTATCATGCGCCGACTG 3180
 QY 3121 ACCTTTCTAGCTTGTCTTGTCCAAATTTGGCTCATCTAGCTATCATGCGCCGACTG 3180

Db 3181 CCGATAACGATACGAATAAATAGCCGAGGCTTCAATCGAATGGCCGATTTAAAAGTT 3240
 QY 3181 CCGATAACGATACGAATAAATAGCCGAGGCTTCAATCGAATGGCCGATTTAAAAGTT 3240
 Db 3241 GGGTTAAGCGTAATATTCCTGATTTTCAAGTTAATACGTAACAATTTGACAATCAAA 3300
 QY 3241 GGGTTAAGCGTAATATTCCTGATTTTCAAGTTAATACGTAACAATTTGACAATCAAA 3300
 Db 3301 TAAGTGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGC 3360
 QY 3301 TAAGTGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGC 3360
 Db 3361 ATGTGCAACGAAGTGTGAGCTGGGCCACGAGATCCTCGCCGACGCTCATCAAGA 3420
 QY 3361 ATGTGCAACGAAGTGTGAGCTGGGCCACGAGATCCTCGCCGACGCTCATCAAGA 3420
 Db 3421 AGGGATCAAGGAGCAGCAACTGTGAGGTGGCCATCGGGGATCGGATGGAATTCAGA 3480
 QY 3421 AGGGATCAAGGAGCAGCAACTGTGAGGTGGCCATCGGGGATCGGATGGAATTCAGA 3480
 Db 3481 TACAGCGGACATGAAGAACCAACAGCCGAAGAATCCAAATATCTAATACGCAACGA 3540
 QY 3481 TACAGCGGACATGAAGAACCAACAGCCGAAGAATCCAAATATCTAATACGCAACGA 3540
 Db 3541 TGATTTGCAACTCAATTAACCAACCAAGACAATAGACTGGAACACGAGCTAAACCATAG 3600
 QY 3541 TGATTTGCAACTCAATTAACCAACCAAGACAATAGACTGGAACACGAGCTAAACCATAG 3600
 Db 3601 GTTTGCTCTTACAGGACGACGACTGCCAGTAACTCATATGTTAGTACCATTAAGATC 3660
 QY 3601 GTTTGCTCTTACAGGACGACGACTGCCAGTAACTCATATGTTAGTACCATTAAGATC 3660
 Db 3661 GACCAATTCAGGACGAGAGCCACAGGCGCAGCAGATGAGGCGGAGGAGGAGC 3720
 QY 3661 GACCAATTCAGGACGAGAGCCACAGGCGCAGCAGATGAGGCGGAGGAGGAGC 3720
 Db 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGCGGAGGAGC 3780
 QY 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGCGGAGGAGC 3780
 Db 3781 AGGAGGCGGCTCGACGCTGATATCATTTATTCATGCAACGAGGATATCTCGATG 3840
 QY 3781 AGGAGGCGGCTCGACGCTGATATCATTTATTCATGCAACGAGGATATCTCGATG 3840
 Db 3841 AATATCCAGCTGATTCCTGCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
 QY 3841 AATATCCAGCTGATTCCTGCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
 Db 3901 ACGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAAATTTTCAATTA 3960
 QY 3901 ACGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAAATTTTCAATTA 3960
 Db 3961 TTGAAAATTAATATTTTGAACAGCTGTATCATATGATTTAATGATGATGATGATGAT 4020
 QY 3961 TTGAAAATTAATATTTTGAACAGCTGTATCATATGATTTAATGATGATGATGATGAT 4020
 Db 4021 TGGCAATTAAGAGATGATCATCTGCCACAAAGACCCATCTGAGGATATTTTACTATA 4080
 QY 4021 TGGCAATTAAGAGATGATCATCTGCCACAAAGACCCATCTGAGGATATTTTACTATA 4080
 Db 4081 TGGACAGAATATTTACGTTTATTTCTTGGAAATTTAATCAAGTGGTGGCGCTCG 4140
 QY 4081 TGGACAGAATATTTACGTTTATTTCTTGGAAATTTAATCAAGTGGTGGCGCTCG 4140
 Db 4141 GCTTCAAGTGTACTTACCAACGCGTGTGGCTCGATTCGATTTGATGATGATGATGAT 4200
 QY 4141 GCTTCAAGTGTACTTACCAACGCGTGTGGCTCGATTCGATTTGATGATGATGATGAT 4200
 Db 4201 GCTTTATCAACTTCGTTGCTTACCTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
 QY 4201 GCTTTATCAACTTCGTTGCTTACCTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
 Db 4261 TGGCAACGTTAAGAGCACTGAGCACCACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320

QY	4261	TGCGAACGTTAAGAGCACTAGACCACTACGTGCGCATGTCGCGTATGCGAGGCAATGAGGG	4320
Db	4321	TCGTCGTTAATGGCTGGTACAGCTATACCGTCCATCTTCAATGTCATTTGGTGTGTC	4380
QY	4321	TCGTCGTTAATGGCTGGTACAGCTATACCGTCCATCTTCAATGTCATTTGGTGTGTC	4380
Db	4381	TAATATTTTGGCTAAATTTTGGCCATATGGGTGTACAGCTTTTGGCTGGAAATATTTTA	4440
QY	4381	TAATATTTTGGCTAAATTTTGGCCATATGGGTGTACAGCTTTTGGCTGGAAATATTTTA	4440
Db	4441	AGTGGAGGACATGAATGCGACCAAGCTCAGCCACGAGATCATACCAATCCCAATGCT	4500
QY	4441	AGTGGAGGACATGAATGCGACCAAGCTCAGCCACGAGATCATACCAATCCCAATGCT	4500
Db	4501	CGGAGAGGAGAACTACACGTGGTGAATTCAGCAATGAATTCGATCATGTAGTAAGC	4560
QY	4501	CGGAGAGGAGAACTACACGTGGTGAATTCAGCAATGAATTCGATCATGTAGTAAGC	4560
Db	4561	CGTATCTGCTTTTCCAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG	4620
QY	4561	CGTATCTGCTTTTCCAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG	4620
Db	4621	CTATCGATTCACGAGAGTGGACAAAGCAACAAATTCGTGAACGACATCATGATTT	4680
QY	4621	CTATCGATTCACGAGAGTGGACAAAGCAACAAATTCGTGAACGACATCATGATTT	4680
Db	4681	TATATTTGCTATCTTCATCATATTTGGATCTTTTTCACACTCAATCTGTTCAATGGTG	4740
QY	4681	TATATTTGCTATCTTCATCATATTTGGATCTTTTTCACACTCAATCTGTTCAATGGTG	4740
Db	4741	TTATCATTTGATAATTTAATGAGCAAAAGAAAAGCAGGTGGATCATTAAGATGTTCA	4800
QY	4741	TTATCATTTGATAATTTAATGAGCAAAAGAAAAGCAGGTGGATCATTAAGATGTTCA	4800
Db	4801	TGACAGAAATCAGAAAAAGTACTATATGCTATGAAAAAGATGGCTCTAAAAAACCAT	4860
QY	4801	TGACAGAAATCAGAAAAAGTACTATATGCTATGAAAAAGATGGCTCTAAAAAACCAT	4860
Db	4861	TAAAGCCATTCACAGCCCAAGGTGGCGACCAACAGCAATAGCTTTTGAATAGTAACCG	4920
QY	4861	TAAAGCCATTCACAGCCCAAGGTGGCGACCAACAGCAATAGCTTTTGAATAGTAACCG	4920
Db	4921	ATAAGAAATTCGATTAATCATATTTATGCTATGCTGTAACATGTTTACCATGACCC	4980
QY	4921	ATAAGAAATTCGATTAATCATATTTATGCTATGCTGTAACATGTTTACCATGACCC	4980
Db	4981	TCGATCGTTACGATCGCTCGGACACGTATTAACCGGCTCCTAGACTATCTCAATGCGAT	5040
QY	4981	TCGATCGTTACGATCGCTCGGACACGTATTAACCGGCTCCTAGACTATCTCAATGCGAT	5040
Db	5041	TCGTAGTATTTTTCAGTTCCGAAATGCTATTAATAAATATTCGTTTACGATATFCAATTT	5100
QY	5041	TCGTAGTATTTTTCAGTTCCGAAATGCTATTAATAAATATTCGTTTACGATATFCAATTT	5100
Db	5101	TTATTTAGCCATGGAATTTATTTGATGTAGTGTTCATTTTATCCATCTTAGTCTTG	5160
QY	5101	TTATTTAGCCATGGAATTTATTTGATGTAGTGTTCATTTTATCCATCTTAGTCTTG	5160
Db	5161	TACTTAGGATATTTATCGAAGTACTTTCGTCGCGGACCTGCTCCGAGTGGTGGTG	5220
QY	5161	TACTTAGGATATTTATCGAAGTACTTTCGTCGCGGACCTGCTCCGAGTGGTGGTG	5220
Db	5221	TGGGAAAGTGGGCGGTGCTCTTCGACTTGGTGAAGGGAGCCAAAGGCAATTCGGACATGC	5280
QY	5221	TGGGAAAGTGGGCGGTGCTCTTCGACTTGGTGAAGGGAGCCAAAGGCAATTCGGACATGC	5280
Db	5281	TCCTCGCTGGCCATGTCGCTCGCGGCTGTTTCAACATCTGCTGCTGTTCTCTGG	5340
QY	5281	TCCTCGCTGGCCATGTCGCTCGCGGCTGTTTCAACATCTGCTGCTGTTCTCTGG	5340
Db	5341	TCATGTTTCATCTTTGCCATTTTTCGGCATGTCGTTCTTCATGCACTGAGGAGAGCG	5400

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Db	1381	CGGAAGAGTGCCTCCGCGCCAAAGCGGCCAAGCTGGAGAGCGGGCCAAATGCGAGGCTC	1440
Qy	1381	CGGAAGAGTGCCTCCGCGCCAAAGCGGCCAAGCTGGAGAGCGGGCCAAATGCGAGGCTC	1440
Db	1441	AGGACAGCGGATGGCGTCCGCGCGAAGAGGCTGCATGCTATCGGAAATGGCCAAAG	1500
Qy	1441	AGGACAGCGGATGGCGTCCGCGCGAAGAGGCTGCATGCTATCGGAAATGGCCAAAG	1500
Db	1501	GTCCGAGCTATTCCTGATGATGAGCTATTTGTTGGCGCGAGAGGCAACGATG	1560
Qy	1501	GTCCGAGCTATTCCTGATGATGAGCTATTTGTTGGCGCGAGAGGCAACGATG	1560
Db	1561	ACACACAAAGAGAGATGTCATTCGGAGCGTCGAGGTGGAGTGGGATCGGTGAGCG	1620
Qy	1561	ACACACAAAGAGAGATGTCATTCGGAGCGTCGAGGTGGAGTGGGATCGGTGAGCG	1620
Db	1621	TTATACAAAGACACACAGCCTACACAGACACACCAAGCTACCAAGTTCGTAAGTGA	1680
Qy	1621	TTATACAAAGACACACAGCCTACACAGACACACCAAGCTACCAAGTTCGTAAGTGA	1680
Db	1681	GCACAGATCCTTATCCTTACCTGCTTCCCGTTTAAACATACGAGGAGATCAGTAGTT	1740
Qy	1681	GCACAGATCCTTATCCTTACCTGCTTCCCGTTTAAACATACGAGGAGATCAGTAGTT	1740
Db	1741	CTCACAAATACAGATACGGAACGAGCGTGGCGCTTTGGTATACCGGATAGCATGTA	1800
Qy	1741	CTCACAAATACAGATACGGAACGAGCGTGGCGCTTTGGTATACCGGATAGCATGTA	1800
Db	1801	AGCCATGTTATGTCACATATCAGGATGCCAGACGACTTGCCTTATGCCAGGACT	1860
Qy	1801	AGCCATGTTATGTCACATATCAGGATGCCAGACGACTTGCCTTATGCCAGGACT	1860
Db	1861	CGAATCGCTCAGCCGATGTCGGAAGAGATGGGGCATATAGTCCCGTGTACTATG	1920
Qy	1861	CGAATCGCTCAGCCGATGTCGGAAGAGATGGGGCATATAGTCCCGTGTACTATG	1920
Db	1921	GCAATCTAGCTCCGACACTATCTATACCTCGCATCAGTCCCGAATATCGTATACCT	1980
Qy	1921	GCAATCTAGCTCCGACACTATCTATACCTCGCATCAGTCCCGAATATCGTATACCT	1980
Db	1981	CACATGCGATCTACTCGCGGATGCGCGTATGCGGCTGACACATGACCAAGGAGA	2040
Qy	1981	CACATGCGATCTACTCGCGGATGCGCGTATGCGGCTGACACATGACCAAGGAGA	2040
Db	2041	GCAATTCGCGAAGCGGACACAGCAATCAATCAGTGGCGCCCAATGCGGCACCA	2100
Qy	2041	GCAATTCGCGAAGCGGACACAGCAATCAATCAGTGGCGCCCAATGCGGCACCA	2100
Db	2101	CCTGCTGGACACCAATCACAAGCTCGATCATCGGACTACGAAATGCGCTGAGTGA	2160
Qy	2101	CCTGCTGGACACCAATCACAAGCTCGATCATCGGACTACGAAATGCGCTGAGTGA	2160
Db	2161	CGGAGAGCTGGCAAGATTAACATCATGACATCTTTTATCGAGCCCGTCCAGACAC	2220
Qy	2161	CGGAGAGCTGGCAAGATTAACATCATGACATCTTTTATCGAGCCCGTCCAGACAC	2220
Db	2221	AAACGGTGGTATGATGAAGATGTGATGGTCTTGAATGATCATCGAAGCGCGCTG	2280
Qy	2221	AAACGGTGGTATGATGAAGATGTGATGGTCTTGAATGATCATCGAAGCGCGCTG	2280
Db	2281	GTCCGACAGTCCGCGAAGCGATCCGCGTGTCTCGTTTACTATTTCCCAACAGAGGAG	2340
Qy	2281	GTCCGACAGTCCGCGAAGCGATCCGCGTGTCTCGTTTACTATTTCCCAACAGAGGAG	2340
Db	2341	ATGACGAGATGGCGGAGCTTCAAGAGACAGGCACTCGAAGTATCGTCAAGGCAATG	2400
Qy	2341	ATGACGAGATGGCGGAGCTTCAAGAGACAGGCACTCGAAGTATCGTCAAGGCAATG	2400
Db	2401	ATGTGTTTGTGTGGGACTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2460
Qy	2401	ATGTGTTTGTGTGGGACTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2460
Db	2461	TCATCGTCTTCGATCCCTCGTCCGAGCTCTTCATCAGCGTGTGCAATGTTGGTCAACGA	2520
Qy	2461	TCATCGTCTTCGATCCCTCGTCCGAGCTCTTCATCAGCGTGTGCAATGTTGGTCAACGA	2520
Db	2521	TGTTTATGCAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2580
Qy	2521	TGTTTATGCAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2580
Db	2581	GCAACTATTTCTTCACCGCCACCTTTGCCATCGAGCCACCATGAAGCTAATGGCCATGA	2640
Qy	2581	GCAACTATTTCTTCACCGCCACCTTTGCCATCGAGCCACCATGAAGCTAATGGCCATGA	2640
Db	2641	GCCTTATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA	2700
Qy	2641	GCCTTATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA	2700
Db	2701	CGCTTATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA	2760
Qy	2701	CGCTTATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA	2760
Db	2761	TGCTGCGTGTATTCACAACTGGCCAAAGTCTTGGCCCACTTAATTTACTCATTTCA	2820
Qy	2761	TGCTGCGTGTATTCACAACTGGCCAAAGTCTTGGCCCACTTAATTTACTCATTTCA	2820
Db	2821	TGGGACGACCATGGCGCTTGGGTATCTGACATTTGTACTTTGCATTTATCATCTCA	2880
Qy	2821	TGGGACGACCATGGCGCTTGGGTATCTGACATTTGTACTTTGCATTTATCATCTCA	2880
Db	2881	TCCTTTCGCGTGTATGGAATGCAACTGTTGGGAAAGAAATATCATGATCACAAGCGCT	2940
Qy	2881	TCCTTTCGCGTGTATGGAATGCAACTGTTGGGAAAGAAATATCATGATCACAAGCGCT	2940
Db	2941	TTCCGGATGGGACCTGGCGCTGGGACTTTCAGGACTTATGCACAGCTTTCATGATCG	3000
Qy	2941	TTCCGGATGGGACCTGGCGCTGGGACTTTCAGGACTTATGCACAGCTTTCATGATCG	3000
Db	3001	TGTTCCGGTGTCTCTCGGAGAAATGGATCGAGTCCATGTTGGGACTGATGATGATGATG	3060
Qy	3001	TGTTCCGGTGTCTCTCGGAGAAATGGATCGAGTCCATGTTGGGACTGATGATGATGATG	3060
Db	3061	ATGTCGCTGATTCCTTCTTGGCCACCGTGTCTGATCGGCAATCTTGTGGTACTTA	3120
Qy	3061	ATGTCGCTGATTCCTTCTTGGCCACCGTGTCTGATCGGCAATCTTGTGGTACTTA	3120
Db	3121	ACCTTTCTTAGCTTGTCTTGTCCAAATTTGGCTCATCTAGCTTATCAGCGCGACTG	3180
Qy	3121	ACCTTTCTTAGCTTGTCTTGTCCAAATTTGGCTCATCTAGCTTATCAGCGCGACTG	3180
Db	3181	CCGATACGATACGATACGATACGATACGATACGATACGATACGATACGATACGAT	3240
Qy	3181	CCGATACGATACGATACGATACGATACGATACGATACGATACGATACGATACGAT	3240
Db	3241	GGGTTAAGCGTAAATATGCTGATTTTCAAGTAAATGATGATGATGATGATGATGAT	3300
Qy	3241	GGGTTAAGCGTAAATATGCTGATTTTCAAGTAAATGATGATGATGATGATGATGAT	3300
Db	3301	TAACTGATACGATACGATACGATACGATACGATACGATACGATACGATACGAT	3360
Qy	3301	TAACTGATACGATACGATACGATACGATACGATACGATACGATACGATACGAT	3360
Db	3361	ATGTTGACCAAGAACTGGAGTGGCCACGAGATCTTCGCGGACGGCTTCATCAAG	3420
Qy	3361	ATGTTGACCAAGAACTGGAGTGGCCACGAGATCTTCGCGGACGGCTTCATCAAG	3420
Db	3421	AGGGATCAAGGAGACGACGACGACGACGACGACGACGACGACGACGACGACGAC	3480
Qy	3421	AGGGATCAAGGAGACGACGACGACGACGACGACGACGACGACGACGACGACGAC	3480
Db	3481	TACACGGGACATGAAGAACCAAGCGGAGAAATCCAAATATCTAAATACGCAACGA	3540
Qy	3481	TACACGGGACATGAAGAACCAAGCGGAGAAATCCAAATATCTAAATACGCAACGA	3540
Db	3541	TGATTTGGCACTCAATTTAACCCCAAGCAATAGCTGGAACAGGACTAAACCATAGAG	3600
Qy	3541	TGATTTGGCACTCAATTTAACCCCAAGCAATAGCTGGAACAGGACTAAACCATAGAG	3600

QY 3541 TGATTGGCAACTCAATTAACCAACCAAGACAATAGACTGGAACACAGAGCTAAACCATAGAG 3600
Db 3601 GTTTCCTCTTACAGGACGACGACACTGCCAGCATTAACATCATATGCTAGCCATAGAATC 3660
QY 3601 GTTTCCTCTTACAGGACGACGACACTGCCAGCATTAACATCATATGCTAGCCATAGAATC 3660
Db 3661 GACCATTCAAGGACGAGACCCACAAAGGCGCCGAGACGATGAGGCGGAGGAGAAC 3720
QY 3661 GACCATTCAAGGACGAGACCCACAAAGGCGCCGAGACGATGAGGCGGAGGAGAAC 3720
Db 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAAGTGGACGAGGAGGCGGAATCG 3780
QY 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAAGTGGACGAGGAGGCGGAATCG 3780
Db 3781 AGGAGGCGCGCTCGACGCTGATATCATTTATCATGCAACACGAGGATATACTCGATG 3840
QY 3781 AGGAGGCGCGCTCGACGCTGATATCATTTATCATGCAACACGAGGATATACTCGATG 3840
Db 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
QY 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
Db 3901 AGGATGACTCCCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3960
QY 3901 AGGATGACTCCCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3960
Db 3961 TTGAAATAAATATTTTGAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTT 4020
QY 3961 TTGAAATAAATATTTTGAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTT 4020
Db 4021 TGGCATTAGAAGATGATCATCTGCCAAGACCCATCTACTGAGGATATTTTACTATA 4080
QY 4021 TGGCATTAGAAGATGATCATCTGCCAAGACCCATCTACTGAGGATATTTTACTATA 4080
Db 4081 TGGCAGAAATATTTACGGTTATTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTG 4140
QY 4081 TGGCAGAAATATTTACGGTTATTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTG 4140
Db 4141 GCTTCAAAAGTGACTTCAACACGCTGGTGTGGCTCGATTCGATTCGATTCATGGTAT 4200
QY 4141 GCTTCAAAAGTGACTTCAACACGCTGGTGTGGCTCGATTCGATTCGATTCATGGTAT 4200
Db 4201 GCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATCAAGCTTCAAGACTA 4260
QY 4201 GCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATCAAGCTTCAAGACTA 4260
Db 4261 TCGCAACGTTAAGACGACTGAGACCACTACGTGCCATGTCCCGTATGAGGCGCATGAGG 4320
QY 4261 TCGCAACGTTAAGACGACTGAGACCACTACGTGCCATGTCCCGTATGAGGCGCATGAGG 4320
Db 4321 TCGTGGTTAATCGCTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380
QY 4321 TCGTGGTTAATCGCTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380
Db 4381 TAATATTTGGCTAATTTTGGCAATAATGGGTGTACAGCTTTTCTGGGAAATATTTTA 4440
QY 4381 TAATATTTGGCTAATTTTGGCAATAATGGGTGTACAGCTTTTCTGGGAAATATTTTA 4440
Db 4441 AGTGGAGGACATGAATGCGACGAAGCTCAGCCAGAGATCATACCAATCGCAATGCT 4500
QY 4441 AGTGGAGGACATGAATGCGACGAAGCTCAGCCAGAGATCATACCAATCGCAATGCT 4500
Db 4501 GCGAGGCGGAGAACTACAGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAG 4560
QY 4501 GCGAGGCGGAGAACTACAGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAG 4560
Db 4561 GCTATCTGCGCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGTAACGATG 4620
QY 4561 GCTATCTGCGCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGTAACGATG 4620
Db 4621 CTATCGATTACGAGGTTGGAACCAACCAATTCGTTGAAACGCAATCTACATGAT 4680
QY 4621 CTATCGATTACGAGGTTGGAACCAACCAATTCGTTGAAACGCAATCTACATGAT 4680

Db 4681 TATATTTCTGTTATCTTCATCATATTTTGATCTCTTTTTCACACTCAATCTGTTCTTGGT 4740
QY 4681 TATATTTCTGTTATCTTCATCATATTTTGATCTCTTTTTCACACTCAATCTGTTCTTGGT 4740
Db 4741 TATATTTCTGTTATCTTCATCATATTTTGATCTCTTTTTCACACTCAATCTGTTCTTGGT 4800
QY 4741 TATATTTCTGTTATCTTCATCATATTTTGATCTCTTTTTCACACTCAATCTGTTCTTGGT 4800
Db 4801 TGACAGAGATCAGAAAAGTACTATATGCTATGAAAAGATGGCTCTTAAAAAACCAT 4860
QY 4801 TGACAGAGATCAGAAAAGTACTATATGCTATGAAAAGATGGCTCTTAAAAAACCAT 4860
Db 4861 TAAAGCCATTCCAAAGACCAAGGTGGCCACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
QY 4861 TAAAGCCATTCCAAAGACCAAGGTGGCCACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
Db 4921 ATAGAAATTCGATATATATATGTTATGTTTCAATGTTGCTGAACATGTTACCATGAGCC 4980
QY 4921 ATAGAAATTCGATATATATATGTTATGTTTCAATGTTGCTGAACATGTTACCATGAGCC 4980
Db 4981 TCGATCGTTAGATCGCTCGACAGTATACGCGGTCTAGACTATCTCAATGCGATAT 5040
QY 4981 TCGATCGTTAGATCGCTCGACAGTATACGCGGTCTAGACTATCTCAATGCGATAT 5040
Db 5041 TCGTAGTTATTTTTCAGTTCCGAATGCTTATTAATAATATTCGCTTTACGATATCACTATT 5100
QY 5041 TCGTAGTTATTTTTCAGTTCCGAATGCTTATTAATAATATTCGCTTTACGATATCACTATT 5100
Db 5101 TATTTAGCCCATGGAATTTATTTGATGATGATGTTGCTTATTCATCTTAGTCTTTG 5160
QY 5101 TATTTAGCCCATGGAATTTATTTGATGATGATGTTGCTTATTCATCTTAGTCTTTG 5160
Db 5161 TACTTAGGATATATCGAAGTACTTCTGTCGCCACCTGCTCGAGTGGTGGCTG 5220
QY 5161 TACTTAGGATATATCGAAGTACTTCTGTCGCCACCTGCTCGAGTGGTGGCTG 5220
Db 5221 TGGCGAAAGTGGCGCTGCTTCCGACTGGTGAAGGGAGCCAAAGGCAATTCGGACACTGC 5280
QY 5221 TGGCGAAAGTGGCGCTGCTTCCGACTGGTGAAGGGAGCCAAAGGCAATTCGGACACTGC 5280
Db 5281 TCTTCGCTTTGGCCATGTCGCTGCGGCCCTGTTCAACATCTGCTGCTGTTCTGG 5340
QY 5281 TCTTCGCTTTGGCCATGTCGCTGCGGCCCTGTTCAACATCTGCTGCTGTTCTGG 5340
Db 5341 TCATGTTTCTTTGCCATTTTCCGACTGCTGTTCTTCAACGCTGAAGGAGAGAGCG 5400
QY 5341 TCATGTTTCTTTGCCATTTTCCGACTGCTGTTCTTCAACGCTGAAGGAGAGAGCG 5400
Db 5401 GCATTAAACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTGCTTTTTCAGA 5460
QY 5401 GCATTAAACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTGCTTTTTCAGA 5460
Db 5461 TGTGACGCTAGCCGTTGGGATGGTGTGAGGCGCATTAATCAATGAGGAGCATGCG 5520
QY 5461 TGTGACGCTAGCCGTTGGGATGGTGTGAGGCGCATTAATCAATGAGGAGCATGCG 5520
Db 5521 ATCCACCGCAGCAGCAAAAGCTATCCGGCAATTTGTTGAGTGGTTCAGCGACCGTTGGAATA 5580
QY 5521 ATCCACCGCAGCAGCAAAAGCTATCCGGCAATTTGTTGAGTGGTTCAGCGACCGTTGGAATA 5580
Db 5581 CGTTTCTCTCTCATACCTAGTATTAAGCTTTTGGATAGTTATTAATATGATGATGCTG 5640
QY 5581 CGTTTCTCTCTCATACCTAGTATTAAGCTTTTGGATAGTTATTAATATGATGATGCTG 5640
Db 5641 TCATTCTCGAAGACTATAGTCAGGCGCATGAGGAGGCTCAACGAGGCTCAACCGAGG 5700
QY 5641 TCATTCTCGAAGACTATAGTCAGGCGCATGAGGAGGCTCAACGAGGCTCAACCGAGG 5700
Db 5701 ACTAGGACATGATCTAGATCTGGCAGCAATTCGATCCGAGGCGACCGAGTACATAC 5760
QY 5701 ACTAGGACATGATCTAGATCTGGCAGCAATTCGATCCGAGGCGACCGAGTACATAC 5760

Db 661 CATGGAATTGGCTGACCTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
Qy 661 CATGGAATTGGCTGACCTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
Db 721 TAGGTAATCTAGACGCCCTGGGAAGCTTTAGGGTCTCGGAGCGGCTTAAAACCGTAGCCA 780
Qy 721 TAGGTAATCTAGACGCCCTGGGAAGCTTTAGGGTCTCGGAGCGGCTTAAAACCGTAGCCA 780
Db 781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGTCAATCGAATCGGTGAAGAACTCTGCCGG 840
Qy 781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGTCAATCGAATCGGTGAAGAACTCTGCCGG 840
Db 841 ATGTGATTATCCTGACCATGTTCTCCCTGTCGGTGTTCGCGTTGATGGCCCTACAGATCT 900
Qy 841 ATGTGATTATCCTGACCATGTTCTCCCTGTCGGTGTTCGCGTTGATGGCCCTACAGATCT 900
Db 901 ATATGGGCGTGTCAACGAGAAGTGCATCAAGAAGTTCGCCGTGAGACGCTTCTTGGGGCA 960
Qy 901 ATATGGGCGTGTCAACGAGAAGTGCATCAAGAAGTTCGCCGTGAGACGCTTCTTGGGGCA 960
Db 961 ATCTGACCGACGAGAACCTGGGACTATCAATCGCAATAGCTTCCAAATGGTATTCCGAGG 1020
Qy 961 ATCTGACCGACGAGAACCTGGGACTATCAATCGCAATAGCTTCCAAATGGTATTCCGAGG 1020
Db 1021 ACGAGGCGATCTCATTTCCGTTATCGGCAATATATCCGGTCCGGGGCAATGCCGACGAGC 1080
Qy 1021 ACGAGGCGATCTCATTTCCGTTATCGGCAATATATCCGGTCCGGGGCAATGCCGACGAGC 1080
Db 1081 ATTACGTGTGCTGACGGGTTTGTCCGAATCCGAATTTGGCTTACACAGCTTTCGATT 1140
Qy 1081 ATTACGTGTGCTGACGGGTTTGTCCGAATTTGGCTTACACAGCTTTCGATT 1140
Db 1141 CGTTCGGATGGCTTCTGTCGGCTTCCGGCTGATGACACAGACTTCTGGGAGGATC 1200
Qy 1141 CGTTCGGATGGCTTCTGTCGGCTTCCGGCTGATGACACAGACTTCTGGGAGGATC 1200
Db 1201 TGTACAGCTGGTGTGCGCGCCCGGACCATGTCATGTCATGCTTTTATAGTCATCA 1260
Qy 1201 TGTACAGCTGGTGTGCGCGCCCGGACCATGTCATGTCATGCTTTTATAGTCATCA 1260
Db 1261 TCTTCTAGGTTCACTCATCTTGTGAAATTTGAAATTTGGCCATTTTGGCCATGTCGTATG 1320
Qy 1261 TCTTCTAGGTTCACTCATCTTGTGAAATTTGAAATTTGGCCATTTTGGCCATGTCGTATG 1320
Db 1321 ACGAATTGCAAGGAGGCGGGAAGAGAGGCTGCGCAAGAGGAGCGGATACGCTGAAG 1380
Qy 1321 ACGAATTGCAAGGAGGCGGGAAGAGAGGCTGCGCAAGAGGAGCGGATACGCTGAAG 1380
Db 1381 CGGAAGAAGCTGCCCGCCCAAGCGGCCAAGCTGGAGAGCGGCCAATGCGCAGGCTC 1440
Qy 1381 CGGAAGAAGCTGCCCGCCCAAGCGGCCAAGCTGGAGAGCGGCCAATGCGCAGGCTC 1440
Db 1441 AGGCAGACGGATCGGCTGCCCGCGGAGAGGCTGCACTGCATCCGGAATGGCCAGA 1500
Qy 1441 AGGCAGACGGATCGGCTGCCCGCGGAGAGGCTGCACTGCATCCGGAATGGCCAGA 1500
Db 1501 GTCCAGCATATTCTTGCAATGAGCTATTGTTGGCGGCGAGAGGCAACGATG 1560
Qy 1501 GTCCAGCATATTCTTGCAATGAGCTATTGTTGGCGGCGAGAGGCAACGATG 1560
Db 1561 ACAACAACAAGAGAGATGTCCATTCCGAGGCTCGAGGTGGAGTCGGGTGAGCG 1620
Qy 1561 ACAACAACAAGAGAGATGTCCATTCCGAGGCTCGAGGTGGAGTCGGGTGAGCG 1620
Db 1621 TTATACAAGACACAGCACCTACACAGCACACCAAGCTTACCAAGTTCGTAAGTGA 1680
Qy 1621 TTATACAAGACACAGCACCTACACAGCACACCAAGCTTACCAAGTTCGTAAGTGA 1680
Db 1681 GCACGACATCCTTATCCTTACCTGTTACCGTTTAAACATACGACGAGGGATCACCTAGTT 1740
Qy 1681 GCACGACATCCTTATCCTTACCTGTTTACCGTTTAAACATACGACGAGGGATCACCTAGTT 1740
Db 1741 CTCACAAGTACAGTACGGAACGGACGCTGGCGCTTTGGTATATACCCGCTAGCGATCGTA 1800

Qy 1741 CTCACAAGTACAGTACGGAACGGACGCTGGCCCTTTGGTATATCCCGGTAGCGATCGTA 1800
Db 1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCATTGGCCCTATGCCGACGACT 1860
Qy 1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCATTGGCCCTATGCCGACGACT 1860
Db 1861 CGAATGCCGTCAACCCCGATGTCGAAGAGAATGGGCCCATATAGTGCCCGTGTACTATG 1920
Qy 1861 CGAATGCCGTCAACCCCGATGTCGAAGAGAATGGGCCCATATAGTGCCCGTGTACTATG 1920
Db 1921 GCAATCTAGGCTCCGACACTCATCTATACCTCGCATCAGTCCGGAATATCGTATACCT 1980
Qy 1921 GCAATCTAGGCTCCGACACTCATCTATACCTCGCATCAGTCCGGAATATCGTATACCT 1980
Db 1981 CACATGGCGATCTACTCGGGCGCATGCGCGTCAATGGGGCTCAGCAATATGACAGGAGA 2040
Qy 1981 CACATGGCGATCTACTCGGGCGCATGCGCGTCAATGGGGCTCAGCAATATGACAGGAGA 2040
Db 2041 GCAAATTGCGCAACCGCAACACAGCAATCAATCAGTGGCGCCACCAATGGCGGCACCA 2100
Qy 2041 GCAAATTGCGCAACCGCAACACAGCAATCAATCAGTGGCGCCACCAATGGCGGCACCA 2100
Db 2101 CCTGTCTGGACACCAATCACAAGCTCGATCATCGGACTACGAAATTTGGCTGGAGTCA 2160
Qy 2101 CCTGTCTGGACACCAATCACAAGCTCGATCATCGGACTACGAAATTTGGCTGGAGTCA 2160
Db 2161 CGGACGAGCTGGCAAGATTAAACATCATGACATCTTTTATCGAGCCCTCCAGACAC 2220
Qy 2161 CGGACGAGCTGGCAAGATTAAACATCATGACATCTTTTATCGAGCCCTCCAGACAC 2220
Db 2221 AAACGGTGGTGTATGAAAGATGTGTGCTTCAATGACATCATCAAGAGCGCGTG 2280
Qy 2221 AAACGGTGGTGTATGAAAGATGTGTGCTTCAATGACATCATCAAGAGCGCGTG 2280
Db 2281 GTCGGCAGCTCGGGCAAGCGATCGCGTGTCTCCGTTTACTATTTCCTCAACAGAGGACG 2340
Qy 2281 GTCGGCAGCTCGGGCAAGCGATCGCGTGTCTCCGTTTACTATTTCCTCAACAGAGGACG 2340
Db 2341 ATGAGGAGATGGGCGGACGTTCAAGACAAGGCACTCGAAGTGTATCTCAAGGCACTCG 2400
Qy 2341 ATGAGGAGATGGGCGGACGTTCAAGACAAGGCACTCGAAGTGTATCTCAAGGCACTCG 2400
Db 2401 ATGTGTTTGTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGC 2460
Qy 2401 ATGTGTTTGTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGC 2460
Db 2461 TCATCGCTTTCGATCCCTTCGTCGAGCTTCTCATCACGCTGTGCATTTGTGTCACACGA 2520
Qy 2461 TCATCGCTTTCGATCCCTTCGTCGAGCTTCTCATCACGCTGTGCATTTGTGTCACACGA 2520
Db 2521 TGTTCATGGCAATGGATCACCACGATATGAACAGGAGATGGAACGCGTCTCAAGAGTG 2580
Qy 2521 TGTTCATGGCAATGGATCACCACGATATGAACAGGAGATGGAACGCGTCTCAAGAGTG 2580
Db 2581 GCAACTATTTCTTCAACCCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
Qy 2581 GCAACTATTTCTTCAACCCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
Db 2641 GCGCCCAAGTACTATTTCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
Qy 2641 GCGCCCAAGTACTATTTCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
Db 2701 CGCTATTGGAACTGGGACTCGAGGGTCTCGGATTTGGCTTCCCTTTCCAT 2760
Qy 2701 CGCTATTGGAACTGGGACTCGAGGGTCTCGGATTTGGCTTCCCTTTCCAT 2760
Db 2761 TGCTCGGTATTCAAACCTGGCAGTCTTGCCCACTTAAATTTACTCATTTTCGATTA 2820
Qy 2761 TGCTCGGTATTCAAACCTGGCAGTCTTGCCCACTTAAATTTACTCATTTTCGATTA 2820
Db 2821 TGGGACGACCATGGGCGCTTTGGGTAATGTGACATTTGTACTTTGCATTTATCATCTTCA 2880

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QY	2821	TGGAGCACCATTGGCGCTTTGGGTAATCTGACAAATTTGTACTTTTGCATTAATCATCTTCA	2880
Db	2881	TCCTTGGGTTGATGGAATGCAACTCTTCGGAAGAAATATATCATGATCACAGGACCGCT	2940
QY	2881	TCCTTGGGTTGATGGAATGCAACTCTTCGGAAGAAATATATCATGATCACAGGACCGCT	2940
Db	2941	TTCCGGATGGCGACCTGCCGCGTGGAACTTCACCGACATTTATGACAGCTTCATGATCG	3000
QY	2941	TTCCGGATGGCGACCTGCCGCGTGGAACTTCACCGACATTTATGACAGCTTCATGATCG	3000
Db	3001	TGTTCCGGGTGCTCTGCGGAGATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGGG	3060
QY	3001	TGTTCCGGGTGCTCTGCGGAGATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGGG	3060
Db	3061	ATGTCCTGTCGATCCCTCTCTTGTGGCCACCGTTGTCATCGCAATCTTGTGGTACTTA	3120
QY	3061	ATGTCCTGTCGATCCCTCTCTTGTGGCCACCGTTGTCATCGCAATCTTGTGGTACTTA	3120
Db	3121	ACCTTTCTTAGCCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTATACAGCCGACTG	3180
QY	3121	ACCTTTCTTAGCCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTATACAGCCGACTG	3180
Db	3181	CGGATAACGATACGAATAAATAGCCGAGGCTTCAATCGAATTTGGCGATTTAAAGTT	3240
QY	3181	CGGATAACGATACGAATAAATAGCCGAGGCTTCAATCGAATTTGGCGATTTAAAGTT	3240
Db	3241	GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTTAATAGTAAACAAATTGACAAATCAA	3300
QY	3241	GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTTAATAGTAAACAAATTGACAAATCAA	3300
Db	3301	TAAAGTATCAACCATCAGGTGAGAGCAACACAGATCAGTTGGATTTGGAGCGAAGCG	3360
QY	3301	TAAAGTATCAACCATCAGGTGAGAGCAACACAGATCAGTTGGATTTGGAGCGAAGCG	3360
Db	3361	ATGGTGACAAAGGACGACCAACTGGAGTGGCCATCGGGGATCGGATCGGAATTCACGA	3420
QY	3361	ATGGTGACAAAGGACGACCAACTGGAGTGGCCATCGGGGATCGGATCGGAATTCACGA	3420
Db	3421	AGGGGATCAAGGACGACCAACTGGAGTGGCCATCGGGGATCGGATCGGAATTCACGA	3480
QY	3421	AGGGGATCAAGGACGACCAACTGGAGTGGCCATCGGGGATCGGATCGGAATTCACGA	3480
Db	3481	TACAGCGGACATGAAGAACCAACGCGGAGAAATCCAAATATCTTAAATACGCAACGA	3540
QY	3481	TACAGCGGACATGAAGAACCAACGCGGAGAAATCCAAATATCTTAAATACGCAACGA	3540
Db	3541	TGATTGGCACTCAATTAACCAACGACCAATAGAGCTGGAGCAAGCTTAAACCATAGAG	3600
QY	3541	TGATTGGCACTCAATTAACCAACGACCAATAGAGCTGGAGCAAGCTTAAACCATAGAG	3600
Db	3601	GTTTGTCCTTACAGGACGACCACTGCCAGCATTAATCTATGTGTAGCCATAAGATC	3660
QY	3601	GTTTGTCCTTACAGGACGACCACTGCCAGCATTAATCTATGTGTAGCCATAAGATC	3660
Db	3661	GACCATTCAGGACGAGGACCAAGGCGGCGGAGACGATGGAGGCGGAGGAGGAGC	3720
QY	3661	GACCATTCAGGACGAGGACCAAGGCGGCGGAGACGATGGAGGCGGAGGAGGAGC	3720
Db	3721	GGAGCCGACGAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGAGGAGGAGGATCG	3780
QY	3721	GGAGCCGACGAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGAGGAGGAGGATCG	3780
Db	3781	AGGAGGCGCGCTCGACGATATCATTTATTCACGACGAGGAGGATATCTCGATG	3840
QY	3781	AGGAGGCGCGCTCGACGATATCATTTATTCACGACGAGGAGGATATCTCGATG	3840
Db	3841	AATATCAGCTGATTCGTCGCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG	3900
QY	3841	AATATCAGCTGATTCGTCGCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG	3900
Db	3901	ACGATGACTCGCGCTTCTGCGAAGGATGGGCAATTTAGGACTGAAACTTTTCAATTA	3960
QY	3901	ACGATGACTCGCGCTTCTGCGAAGGATGGGCAATTTAGGACTGAAACTTTTCAATTA	3960
Db	3961	TTGAAATAAATAATTTTGAACAGCTGTATCACTATGATTTTAAATGAGTAGCTTAGCTT	4020
QY	3961	TTGAAATAAATAATTTTGAACAGCTGTATCACTATGATTTTAAATGAGTAGCTTAGCTT	4020
Db	4021	TGGCATTAGAAGATCTACATCTGCCACAAAGACCCATCTACGAGGATATTTTATACATA	4080
QY	4021	TGGCATTAGAAGATCTACATCTGCCACAAAGACCCATCTACGAGGATATTTTATACATA	4080
Db	4081	TGGACAGAATATTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG	4140
QY	4081	TGGACAGAATATTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG	4140
Db	4141	GCCTTCAAGTGTACTTCAACCAACGGGTGGTGGCTCGAATTCGTGATTTGTCATGGTAT	4200
QY	4141	GCCTTCAAGTGTACTTCAACCAACGGGTGGTGGCTCGAATTCGTGATTTGTCATGGTAT	4200
Db	4201	CGCTTATCAACTTCGTGCTTCACTTGTGGAGCTGGTGTATTTCAAGCCTTCAAGACTA	4260
QY	4201	CGCTTATCAACTTCGTGCTTCACTTGTGGAGCTGGTGTATTTCAAGCCTTCAAGACTA	4260
Db	4261	TGGCAACGTTAAGAGCACTGAGACCACTAGCTGCCATGTCCCGTATGAGGCGATGAGG	4320
QY	4261	TGGCAACGTTAAGAGCACTGAGACCACTAGCTGCCATGTCCCGTATGAGGCGATGAGG	4320
Db	4321	TCGTCGTTAATGCGCTGGTACAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGC	4380
QY	4321	TCGTCGTTAATGCGCTGGTACAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGC	4380
Db	4381	TAAATATTTTGGCTAATTTTGGCCATAATGGTGTACAGCTTTTGTCTGGAAATATTTTA	4440
QY	4381	TAAATATTTTGGCTAATTTTGGCCATAATGGTGTACAGCTTTTGTCTGGAAATATTTTA	4440
Db	4441	AGTGGAGGACATGAATGGCAGAGCTCAGCCAGAGATCATACCAATCGCAATGCGCT	4500
QY	4441	AGTGGAGGACATGAATGGCAGAGCTCAGCCAGAGATCATACCAATCGCAATGCGCT	4500
Db	4501	GGGAGGCGAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG	4560
QY	4501	GGGAGGCGAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG	4560
Db	4561	CGTATCTGCTCTTCCAAAGTGGCGACCTTCAAAGGCTGGATACAAATCATGAACGATG	4620
QY	4561	CGTATCTGCTCTTCCAAAGTGGCGACCTTCAAAGGCTGGATACAAATCATGAACGATG	4620
Db	4621	CTATCGATTACAGAGAGTGGCAACCAACCAATTCGTTGAACGAACATCTACATGATTT	4680
QY	4621	CTATCGATTACAGAGAGTGGCAACCAACCAATTCGTTGAACGAACATCTACATGATTT	4680
Db	4681	TATATTTCTGTTTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTTCAATGGTG	4740
QY	4681	TATATTTCTGTTTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTTCAATGGTG	4740
Db	4741	TTATCATTTGATATTTTAAATGAGCAACCAACCAATTCGTTGAACGAACATCTACATGATTT	4800
QY	4741	TTATCATTTGATATTTTAAATGAGCAACCAACCAATTCGTTGAACGAACATCTACATGATTT	4800
Db	4801	TGACAGAAGATCGAAGAAAGTACTATATGCTATGAAAGATGGGCTCTAAAAACCAT	4860
QY	4801	TGACAGAAGATCGAAGAAAGTACTATATGCTATGAAAGATGGGCTCTAAAAACCAT	4860
Db	4861	TAAAGCCATTCGAGACCAAGTGGCGACCAACCAATAGTCTTTGAAATAGTAACCG	4920
QY	4861	TAAAGCCATTCGAGACCAAGTGGCGACCAACCAATAGTCTTTGAAATAGTAACCG	4920
Db	4921	ATAAGAAATCGATATATATGTTTATTCATTTGCTTGAACATGTTCCACCATGACCC	4980
QY	4921	ATAAGAAATCGATATATATGTTTATTCATTTGCTTGAACATGTTCCACCATGACCC	4980
Db	4981	TCGATCGTTACGATCGCTCGGACAGCTATAACGCGGCTCTAGACTATCTCAATGCGATAT	5040
QY	4981	TCGATCGTTACGATCGCTCGGACAGCTATAACGCGGCTCTAGACTATCTCAATGCGATAT	5040

D	b	5041	TCGTAGTATTATTTTCAGTTCCGAATGCTATTAATAAATATTTCGCTTTACGATATCACTATT	5100
Q	y	5041	TCGTAGTATTATTTTCAGTTCCGAATGCTATTAATAAATATTTCGCTTTACGATATCACTATT	5100
D	b	5101	TTATTGAGCCATGGAAATTTATTTGATGTAGTAGTGTTCATTTTATCCATCTTAGTCTTG	5160
Q	y	5101	TTATTGAGCCATGGAAATTTATTTGATGTAGTAGTGTTCATTTTATCCATCTTAGTCTTG	5160
D	b	5161	TACTTAGCCGATATTATTCGAGAAGTACTTCGTCTGCCGACCCTGCTCCGAGTGGTGGTG	5220
Q	y	5161	TACTTAGCCGATATTATTCGAGAAGTACTTCGTCTGCCGACCCTGCTCCGAGTGGTGGTG	5220
D	b	5221	TGGCGAAAGTGGCCGTGCTTCGACTGGTGAAGGGAGCCAAAGGCAATCGGACACTGC	5280
Q	y	5221	TGGCGAAAGTGGCCGTGCTTCGACTGGTGAAGGGAGCCAAAGGCAATCGGACACTGC	5280
D	b	5281	TC TTCGGTGGCCATGTCGCTCGCCGCCCTGTTCAAACATCTGCCCTGCTGCTTCTCTTG	5340
Q	y	5281	TC TTCGGTGGCCATGTCGCTCGCCGCCCTGTTCAAACATCTGCCCTGCTGCTTCTCTTG	5340
D	b	5341	TCATGTTTCATCTTTGGCCATTTTCGGCATGTCGCTCTTTCATGCACGCTGAAGGAAGAAGCG	5400
Q	y	5341	TCATGTTTCATCTTTGGCCATTTTCGGCATGTCGCTCTTTCATGCACGCTGAAGGAAGAAGCG	5400
D	b	5401	GCATTAAAGACGCTCTAAACTTCAAGACTTTTGGCCAGAGCATGATCCTGCTCTTTTCAGA	5460
Q	y	5401	GCATTAAAGACGCTCTAAACTTCAAGACTTTTGGCCAGAGCATGATCCTGCTCTTTTCAGA	5460
D	b	5461	TGTCGAGCTCAGCCGCTGGGATGGTGTACTCGAGCCCATATTCAATGAGGAGCATGCG	5520
Q	y	5461	TGTCGAGCTCAGCCGCTGGGATGGTGTACTCGAGCCCATATTCAATGAGGAGCATGCG	5520
D	b	5521	ATCCACCCGACAGCGAAAGGCTATCCGGGCAATTGTGGTTTCAGCGACCGTTGGAATAA	5580
Q	y	5521	ATCCACCCGACAGCGAAAGGCTATCCGGGCAATTGTGGTTTCAGCGACCGTTGGAATAA	5580
D	b	5581	CGTTTCCTCTCATACCTAGTATTAAAGCTTTTTCATAGTTATTAAATATGTACATTGCTG	5640
Q	y	5581	CGTTTCCTCTCATACCTAGTATTAAAGCTTTTTCATAGTTATTAAATATGTACATTGCTG	5640
D	b	5641	TCATTTCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTTAACCGACGACG	5700
Q	y	5641	TCATTTCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTTAACCGACGACG	5700
D	b	5701	ACTACGACATGTACTATGAGATCTGGCAGCAATTTCGATCCGAGGGGACCCAGTACATAC	5760
Q	y	5701	ACTACGACATGTACTATGAGATCTGGCAGCAATTTCGATCCGAGGGGACCCAGTACATAC	5760
D	b	5761	GCTATGATCAGCTGTCGGAATTCCTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAC	5820
Q	y	5761	GCTATGATCAGCTGTCGGAATTCCTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAC	5820
D	b	5821	CGAACAGTACAGATCATATCGATGGACATACCCTATGTCGGGGTACCTCATGTACT	5880
Q	y	5821	CGAACAGTACAGATCATATCGATGGACATACCCTATGTCGGGGTACCTCATGTACT	5880
D	b	5881	CGCTCGACATCTCTCGAGCCCTTACGAAAGACTTCTTTCGCGGAAGGGCAATCCGATAG	5940
Q	y	5881	CGCTCGACATCTCTCGAGCCCTTACGAAAGACTTCTTTCGCGGAAGGGCAATCCGATAG	5940
D	b	5941	AGGAGACGGTGGAGTTGGTGAATAGCGGCCCGCCCGATACGAGGGCTACGAGCCCG	6000
Q	y	5941	AGGAGACGGTGGAGTTGGTGAATAGCGGCCCGCCCGATACGAGGGCTACGAGCCCG	6000
D	b	6001	TCATCATCAAGCTGTGGGTACGCTGAGGAGTACTGGCCCGGGTAAATCCAGCACGCCCT	6060
Q	y	6001	TCATCATCAAGCTGTGGGTACGCTGAGGAGTACTGGCCCGGGTAAATCCAGCACGCCCT	6060
D	b	6061	GGCGAAGACAGGCGCGCGGAGGGAGTGGTCTTTCAGCCGATACGGATCATG	6120
Q	y	6061	GGCGAAGACAGGCGCGCGGAGGGAGTGGTCTTTCAGCCGATACGGATCATG	6120
D	b	6121	CGGATGGCGGTGATCCGGATGTCGGGGACCCCGGCCCGATGAAGACACGACGCCGATG	6180

QY	6121	CGCATGCGGTGATCCGGATGCCGGGGACCCCGCGCCCGATGAAGCAACGACGCGCGATG	6180
Db	6181	CGCCCGCTGCTGGAGATGGTAGTTAAACGGTACTGCAGAGGAGCTGCCGATGCCGATG	6240
QY	6181	CGCCCGCTGCTGGAGATGGTAGTTAAACGGTACTGCAGAGGAGCTGCCGATGCCGATG	6240
Db	6241	AGAGTAATGTAAATAGTCCCGGTGAGGATGACAGCGCGCGCGCGAGCAGCAGCAGCAGCAG	6300
QY	6241	AGAGTAATGTAAATAGTCCCGGTGAGGATGACAGCGCGCGCGCGAGCAGCAGCAGCAGCAG	6300
Db	6301	CGCGCGCGCGCGCGAGCAGCAGCGCGGGGAAGTCCCGGAGCGGGGTAGCCCGGGCGACAGA	6360
QY	6301	CGCGCGCGCGCGCGAGCAGCAGCGCGGGGAAGTCCCGGAGCGGGGTAGCCCGGGCGACAGA	6360
Db	6361	CGCGCGTCTCTGTGGAGAGCGCGGTTCGTGACGAAGAAGCGCCACAAAGTGTGTATCC	6420
QY	6361	CGCGCGTCTCTGTGGAGAGCGCGGTTCGTGACGAAGAAGCGCCACAAAGTGTGTATCC	6420
Db	6421	ACTCGCATCCCGAGCATCACGTCCGCACGCGCGGATGTCTGAGCCAGGCTCGCCCCC	6480
QY	6421	ACTCGCATCCCGAGCATCACGTCCGCACGCGCGGATGTCTGAGCCAGGCTCGCCCCC	6480
Db	6481	CCCTCCAAGATGACCGGAGTATAGCTCTAGA	6513
QY	6481	CCCTCCAAGATGACCGGAGTATAGCTCTAGA	6513
RESULT	4		
ID	US-08-337-339-7	STANDARD; DNA; UNC; 6513 BP.	
AC	xxxxxx		
DT	01-JAN-1900		
DE	Sequence 7, Application US/08337339.		
CC	Sequence 7, Application US/08337339		
CC	Patent No. 5593864		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Warmke, Jeffrey W.		
CC	APPLICANT: Hall, Linda		
CC	APPLICANT: Feng, Gouping		
CC	APPLICANT: Van Der Ploeg, Leonardus		
CC	TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE		
CC	TITLE OF INVENTION: PARA SODIUM CHANNEL		
CC	NUMBER OF SEQUENCES: 7		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: John W. Wallen III		
CC	STREET: P. O. Box 2000, 126 E. Lincoln Avenue		
CC	CITY: Rahway		
CC	STATE: New Jersey		
CC	COUNTRY: USA		
CC	ZIP: 07065-0900		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/337,339		
CC	FILING DATE:		
CC	CLASSIFICATION: 435		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Wallen III, John W.		
CC	REGISTRATION NUMBER: 35,403		
CC	REFERENCE/DOCKET NUMBER: 19332		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: (908) 594-3905		
CC	TELEFAX: (908) 594-4720		
CC	INFORMATION FOR SEQ ID NO: 7:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 6513 base pairs		
CC	TYPE: nucleic acid		
CC	STRANDEDNESS: single		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: CDNA		

Seq	Sequence	6513 BP	1681 A	1548 C	1702 G	1582 T	0 other
Query Match	100.0%	Score 6513	DB 5	Length 6513			
Best Local Similarity	100.0%	Pred. No. 0.00e+00					
Matches	6513	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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1	TCTAGAGTTGGCGCATACAGCAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC	60					
61	GCAGTTTTCCTCCCTTTACCCCGGAATCATTTGGTGCAATTCGACACGATTCGCCG	120					
61	GCAGTTTTCCTCCCTTTACCCCGGAATCATTTGGTGCAATTCGACACGATTCGCCG	120					
121	CTGACATGAAGAAGAGAGAGTGGAAAGAAAGAGAGCGGAGGAGAGGTGCCCGAT	180					
121	CTGACATGAAGAAGAGAGAGTGGAAAGAAAGAGAGCGGAGGAGAGGTGCCCGAT	180					
181	ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGAGGATGAAGTC	240					
181	ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGAGGATGAAGTC	240					
241	CACACCGGATCCTACATTTGAACAGGAGTGGCCAAATACCTGTCGATTCGAGGGCAGCT	300					
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301	TCCCGCGGAATGGCCTCCATCTCTCGAGGATATCGATCCCTTACCTACAGCAATGTAC	360					
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361	TGACATTCGTAGTTGTAAGCAAGGAAAGATATTTTGGCTTTCTGCATCAAAAGCAA	420					
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421	TGTGGATGCTCGATCCATTCGAATCCGATACGTCGTGGCCATTACATTTAGTGCATC	480					
421	TGTGGATGCTCGATCCATTCGAATCCGATACGTCGTGGCCATTACATTTAGTGCATC	480					
481	CATTATTTCCCTATTTCATCATCACCACAAATCTCTGCACTGATGATGATGATGATG	540					
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541	CGACACGCCACCGTTGAGTCCACTCAGTGATATTACCGGAATCTACACATTTGAAT	600					
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601	CAGCTGTTAAAGTGATGCGACGAGGTTTCATTTTATCCCGGTTTACGATCTAGAGATG	660					
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661	CATGGAATGGCTGGACTTCGTAGTATAGCTTTAGCTTATGTGACCATGGGTATAGATT	720					
661	CATGGAATGGCTGGACTTCGTAGTATAGCTTTAGCTTATGTGACCATGGGTATAGATT	720					
721	TAGGTAATCTAGACGCTCGAAGCTTTAGGGTGTGCGAGCGCTTAAACCCGTAGCCA	780					
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781	TTGTGCCAGGCTTGAGACCATCTGTCGCGCGCTCATCGAATCGGTGAAGAATCTGCGG	840					
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841	ATGTGATTTCTTGACCATGTTCTCCCTGTCGGTGTTCGGTGTGATGGCCCTACAGATCT	900					
841	ATGTGATTTCTTGACCATGTTCTCCCTGTCGGTGTTCGGTGTGATGGCCCTACAGATCT	900					
901	ATATGGCGTCTCACCGAAGAGTGCATCAAGAAGTTCCCGCTGGACGGTTCCTGGGCA	960					
901	ATATGGCGTCTCACCGAAGAGTGCATCAAGAAGTTCCCGCTGGACGGTTCCTGGGCA	960					
961	ATCTGACCGAGAACTGGGACTATCACAATCGCAATAGCTCCCAATGGTATTCCGAGG	1020					
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Db 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAAATCCTTTATCGAGCCGCTCCAGACAC 2220
Qy 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAAATCCTTTATCGAGCCGCTCCAGACAC 2220
Db 2221 AAACGGTGGTTCATATGAAGATGTGATGGTCTCTGAATGACATCATCGAAACAGGCCGCTG 2280
Qy 2221 AAACGGTGGTTCATATGAAGATGTGATGGTCTCTGAATGACATCATCGAAACAGGCCGCTG 2280
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Qy 2401 ATGTGTTTGTGTGGGACTGCTCTGGTGTGGTTCGAAATTTTCAGAGTGGGTATCGC 2460
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Qy 2641 GCCCAAGTACTATTTCAGGAGGCTTGGCAATCTTCGATTCATATCGTGGCCCTAT 2700
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Qy 2821 TGGGACGACCATGGGCGCTTTGGTAAATCTGACATTTGTACTTTGCAATTAFCATCTTCA 2880
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Qy 2881 TCCTTTGCGGTGATGGAAATGCAACTGTTCCGGAAGAAATATCATGATCACAGGACCGT 2940
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Qy 2941 TTCGCGATGGGCACTGCCGCGCTTGAACCTTCACCGACTTTATGACAGCTTCATGATCG 3000
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Qy 3121 ACCTTTCTTAGCTTGTCTTCTTCAATTTTGGCTTCATCTAGCTTATCAGGCCGACTG 3180
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Qy 3181 CCGATAACGATACGAATAAAATAGCCGAGGCGCTTCAATCGAAATTTGCGGATTTAAAGTT 3240
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QY 4261 TGGAGCGTTAAGACACTGAGACCAGTACGTGCCATGTCCCGTATGCAGGCGATGAGGG 4320
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Db 4921 ATAAGAAATTCGATATAATCATTTATGTTATGTTGCTGAACATGTTACCATGACCC 4980
QY 4921 ATAAGAAATTCGATATAATCATTTATGTTATGTTGCTGAACATGTTACCATGACCC 4980
Db 4981 TCGATCGTTACGATGCGTCGGACAGTATTAACCGGCTCTAGACTATCTCAATGCGATAT 5040
QY 4981 TCGATCGTTACGATGCGTCGGACAGTATTAACCGGCTCTAGACTATCTCAATGCGATAT 5040
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QY 5041 TCGTAGTTATTTTCAGTTCCGAATGCTATTAATAAATATTTCGTTTACGATATCATATT 5100
Db 5101 TTATTGAGCCATGAATTTATTTGATGTAGTTGTCATTTTATCCATTTAGGCTGTTG 5160
QY 5101 TTATTGAGCCATGAATTTATTTGATGTAGTTGTCATTTTATCCATTTAGGCTGTTG 5160
Db 5161 TACTAGCGATATTATCGAAGTACTTCTGTCGCCGCCCTGCTCCGAGTGGTCCGTTG 5220
QY 5161 TACTAGCGATATTATCGAAGTACTTCTGTCGCCGCCCTGCTCCGAGTGGTCCGTTG 5220
Db 5221 TGGCGAAAGTGGCGGTGTCCTTCGACTGGTGAAGGAGGAGGAGGATTCGACACTGC 5280
QY 5221 TGGCGAAAGTGGCGGTGTCCTTCGACTGGTGAAGGAGGAGGAGGATTCGACACTGC 5280
Db 5281 TCTTCGCGTTGGCCATGTCGTCGCGGCCCTGTTCAACATCTGCTGCTGCTGTTCTG 5340
QY 5281 TCTTCGCGTTGGCCATGTCGTCGCGGCCCTGTTCAACATCTGCTGCTGCTGTTCTG 5340
Db 5341 TCAATGTTATCTTTTGGCCATTTTTCGCGATGTCTGCTTCTTCATGCGATGGAAGAGGCG 5400
QY 5341 TCAATGTTATCTTTTGGCCATTTTTCGCGATGTCTGCTTCTTCATGCGATGGAAGAGGCG 5400

Db 5401 GCATTAAACGAGCTCTACAACCTTTCAGACCTTTGGCAGAGCATGATCCTGCTCTTTTCAGA 5460
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Db 5461 TGTGCGAGCTCAGCCGGTTGGGATGTTGCTACTGTGACGCCATTATCAATGAGGAAGCATGG 5520
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Db 5521 ATCCACCCGACAGCGACAAAGGCTATCCGGGCAATTTGGTTCAGCGACCGTTGGAATAA 5580
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Db 5581 CGTTTCTCTCTCATACCTAGTTTATAGCTTTTGTAGTATTATTAATATGTACATPGCTG 5640
QY 5581 CGTTTCTCTCTCATACCTAGTTTATAGCTTTTGTAGTATTATTAATATGTACATPGCTG 5640
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QY 5821 CGAACAAGTACAAAGATCATATCGATGGACATACCATCTGTCGCGGTGACCTCATGTACT 5880
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QY 5881 GCGTGCACATCTCGACGCCCTTACGAAAGACTTCTTTTCCGCGGAAGGCAATCCGATAG 5940
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QY 5941 AGGAGACGGGTGAGATGTTGAGATAGCGGCCGCCCGATACGAGAGGCTACGAGCCG 6000
Db 6001 TCTCATCAACGCTGTGGCTGAGGAGTACTGCGCCGCGCTATTCAGCACGCGCT 6060
QY 6001 TCTCATCAACGCTGTGGCTGAGGAGTACTGCGCCGCGCTATTCAGCACGCGCT 6060
Db 6061 GCGGAAAGCAACAGCGCGCGGAGAGTGGTCTTTTGGCCGGATACGAGTACG 6120
QY 6061 GCGGAAAGCAACAGCGCGCGGAGAGTGGTCTTTTGGCCGGATACGAGTACG 6120
Db 6121 GCGATGCGGTGATCCGGATGCGCGGGACCCCGCGCGCTGATGAACGAGCGGCGATG 6180
QY 6121 GCGATGCGGTGATCCGGATGCGCGGGACCCCGCGCGCTGATGAACGAGCGGCGATG 6180
Db 6181 CGCCCGTGTGGAGATGTTAAGCTTAACTGAGTACTGCGCGCGCTTAACTCCAGCAGCTG 6240
QY 6181 CGCCCGTGTGGAGATGTTAAGCTTAACTGAGTACTGCGAGAGGCTGCGGATGCGGATG 6240
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QY 6241 AGAGTAAATGTAATGTCGCGGTGAGGATCAGCGCGCGCGGCGAGCAGCAGCAGCAG 6300
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Db 6481 CCTCCAGATGACGCGAGTATTAGCTCTAGA 6513
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Qy 6481 CCTCCAGATGACGCGAGTATTAGCTCTAGA 6513

RESULT 5
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application US/08238163.
CC Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
CC DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238,163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307E-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: misc.feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "Deduced amino acid
CC OTHER INFORMATION: sequence of PGIP from bean."
SQ Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;

Query Match 0.6%; Score 41; DB 5; Length 215;
Best Local Similarity 15.8%; Pred. No. 1.44e-10;
Matches 30; Conservative 77; Mismatches 83; Indels 2; Gaps 2;

Db 22 AKKDGNTSSWTTCCNRTGWGCDTDTTYRVNNDGSHKYSANYNNGNNVGAARKTHY 81
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Qy 1257 ATCACTCTCTAGTTCATCTATCTGTGAATTGATTTGGCCATGTTCCCATGCG 1316
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Qy 1377 GAAGCGGAAGAAGCTGCCCGCCCAAGCGCGCAAGCTGGAG-GAGCGGCGCAATGCGCA 1435

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RESULT 6
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application US/08238163.
CC Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
CC DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238,163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307E-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: misc.feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "Deduced amino acid
CC OTHER INFORMATION: sequence of PGIP from bean."
SQ Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;

Query Match 0.6%; Score 36; DB 5; Length 215;
Best Local Similarity 16.9%; Pred. No. 1.63e-07;
Matches 27; Conservative 61; Mismatches 72; Indels 0; Gaps 0;

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Cp 233 ATCTCTGCTCCGTCGATCATATCGGATTTCTTTTGTTCGACCATATCGCGG 174
| : | : || : : : | : | : : | : : : | : : : | : : :
Db 61 YSSANYTGNNGNVGAARKTHYTHNVSGADSKTVDSYNAGSYSSNGTGNRSGADSY 120
| : | : || : : : | : | : : | : : : | : : : | : : :
Cp 173 CACCTCTCCCTCGGCTCTCTTCTTCCAGCTCCTCTCTGCTTTCATGTTTCAGCGCAAT 114
| : | : || : : : | : | : : | : : : | : : : | : : :
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[illegible]

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CC      COUNTRY: USA
CC      ZIP: 92101-2926
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: DOS
CC      SOFTWARE: FastSeq Version 1.5
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/404,354B
CC      FILING DATE: 15-FEB-1995
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/314,083
CC      FILING DATE: 28-SEP-1994
CC      APPLICATION NUMBER: US 07/914,231
CC      FILING DATE: 13-JUL-1992
CC      APPLICATION NUMBER: US 07/603,751
CC      FILING DATE: 08-NOV-1990
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Seidman, Stephanie L
CC      REGISTRATION NUMBER: 33,779
CC      REFERENCE/DOCKET NUMBER: 6362-53192
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 619-238-0999
CC      TELEFAX: 619-238-0062
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 1:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 5975 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: cDNA
CC      FEATURE:
CC      NAME/KEY: Coding Sequence
CC      LOCATION: 79...5700
CC      OTHER INFORMATION:
CC      Query Match          0.6%; Score 37; DB 6; Length 5975;
CC      Best Local Similarity 65.0%; Pred.No. 4.09e+08;
CC      Matches            80; Conservative    0; Mismatches   43; Indels    0; Gaps    0;

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QY     5367 ATG 5369

RESULT  10
ID     US-08-338-702-1 STANDARD; DNA; UNC; 33 BP.
AC     XXXXXX
DE     01-JAN-1900
Sequence 1, Application US/08338702.
CC     Patent No. 5550049
CC     GENERAL INFORMATION:
CC     APPLICANT: Warmke, Jeffrey W.
CC     APPLICANT: van Der Ploeg, Leonardus
CC     TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC     NUMBER OF SEQUENCES: 7
CC     CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: John W. Wallen III
CC     STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC     CITY: Rahway
CC     STATE: New Jersey
CC     COUNTRY: USA
CC     ZIP: 07065-0907
CC     COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.25
CC     CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: PCT/US95/14378
CC     FILING DATE:
CC     CLASSIFICATION:
CC     ATTORNEY/AGENT INFORMATION:
CC     NAME: Meredith, Roy D.
CC     REGISTRATION NUMBER: 30,777
CC     REFERENCE/DOCKET NUMBER: 19332 PCT
CC     TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (908) 594-4678

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US-08-554-424-7.rni

Tue Oct 14 14:18:09 1997

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CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cdna
CC Sequence 33 BP; 10 A; 8 C; 9 G; 6 T; 0 other;
SQ Query Match 0.5%; Score 30; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.80e-04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCTAGACGTTGGCGCATAGACAATGACAG 30

RESULT 12
ID PCT-US95-14262-1 STANDARD; DNA; UNC; 33 BP.
AC xxxxxx
DE 01-JAN-1900
DE Sequence 1, Application PC/TUS9514262.
CC Sequence 1, Application PC/TUS9514262
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Jack L. Tribble
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: PCT/US95/14262
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Tribble, Jack L.
CC REGISTRATION NUMBER: 32,633
CC REFERENCE/DOCKET NUMBER: 19338 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-5321
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cdna
CC Sequence 33 BP; 10 A; 8 C; 9 G; 6 T; 0 other;
SQ Query Match 0.5%; Score 30; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.80e-04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 TCTAGACGTTGGCGCATAGACAATGACAG 33
QY 1 TCTAGACGTTGGCGCATAGACAATGACAG 30

RESULT 13
ID PCT-US95-14262-1 STANDARD; DNA; UNC; 33 BP.
AC xxxxxx
DE 01-JAN-1900
DE Sequence 1, Application PC/TUS9514262.
CC Sequence 1, Application PC/TUS9514262
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: John W. Wallen III
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0900
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/337,339
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wallen III, John W.
CC REGISTRATION NUMBER: 35,403
CC REFERENCE/DOCKET NUMBER: 19332
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cdna
CC Sequence 33 BP; 10 A; 8 C; 9 G; 6 T; 0 other;
SQ Query Match 0.5%; Score 30; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.80e-04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 TCTAGACGTTGGCGCATAGACAATGACAG 33
QY 1 TCTAGACGTTGGCGCATAGACAATGACAG 30

RESULT 14
ID US-08-237-716-6 STANDARD; DNA; UNC; 75 BP.
AC xxxxxx
DE 01-JAN-1900
DE Sequence 6, Application US/08237716.
CC Sequence 6, Application US/08237716
CC Patent No. 5589384
CC GENERAL INFORMATION:
CC APPLICANT: LIPSCOMBE, Martin J
CC APPLICANT: CHARLES, Ian G
CC APPLICANT: FAIRWEATHER, Neil F
CC TITLE OF INVENTION: FUSION PROTEINS
CC NUMBER OF SEQUENCES: 11
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon & Vanderhye, P.C.
CC STREET: 1100 No. 5589384th Glebe Road, 8th Floor
CC CITY: Arlington
CC STATE: Virginia

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CC COUNTRY: USA
CC ZIP: 22201
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/237,716
CC FILING DATE: 02-MAY-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/896,003
CC FILING DATE: 11-JUN-1992
CC APPLICATION NUMBER: GB 9112553.4
CC FILING DATE: 11-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wilson, Mary J
CC REGISTRATION NUMBER: 32,955
CC REFERENCE/DOCKET NUMBER: 117-157
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-816-4000
CC TELEFAX: 703-816-4100
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 75 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC ANTI-SENSE: YES
CC
SQ Sequence 75 BP; 4 A; 28 C; 34 G; 9 T; 0 other;
Query Match 0.5%; Score 31; DB 5; Length 75;
Best Local Similarity 71.8%; Pred. No. 1.32e-04;
Matches 51; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 2 TAGTCGGCTGCGGAGCGCGCGCTCCGCGTCCGCGTGGCGGCTGCGCGGCTGCGGGA 61
QY 6254 TAGTCGGGTGAGGTGACGCGCGCGCGCAGCAGCAGCAGCAGCGCGGCGGG 6313
Db 62 CCGCGTGGCGG 72
QY 6314 CACGACGCGG 6324

RESULT 15
ID US-08-276-151-6 STANDARD; DNA; UNC; 1213 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 6, Application US/08276151.
CC Sequence 6, Application US/08276151
CC Patent No. 5597719
CC GENERAL INFORMATION:
CC APPLICANT: Freed, Ellen
CC APPLICANT: Ruggieri, Rosamaria
CC TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cooley Godward et al.
CC STREET: Five Palo Alto Square
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,151
CC FILING DATE: 14-JUL-1994
CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Torchia, Ph.D., Timothy E
CC REGISTRATION NUMBER: 36,700
CC REFERENCE/DOCKET NUMBER: ONYX-005/00US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 843-5481
CC TELEFAX: (415) 857-0663
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1213 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC HYPOTHETICAL: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 373..1113
SQ Sequence 1213 BP; 346 A; 299 C; 321 G; 247 T; 0 other;
Query Match 0.5%; Score 30; DB 5; Length 1213;
Best Local Similarity 76.8%; Pred. No. 4.80e-04;
Matches 43; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 29 GCCGGGTAGTCGGCGCGCGCGCGCGCTGCGAGCCACTGCGAGGCACGCGCTGC 84
Cp 6325 GCCGTCGTCGTGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6270

Search completed: Sat Oct 11 05:24:30 1997
Job time : 637 secs.

MRP (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat Oct 11 05:24:49 1997; MasPar time 3089.90 Seconds
Tabular output not generated. 1159.363 Million cell updates/sec

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Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTAGACGTTGGCGCATAG.....ACGCGAGTATTAGCTCTAGA 6513
Comp: AGATCTGCACCGCGGTATC.....TGGCGTCATATCGAGATCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 932594 seqs, 275012777 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-pending
1: PCT91 2: PCT92 3: PCT93 4: PCT94 5: PCT95 6: PCT96 7: PCT97
8: 075 9: 076 10: 077 11: 0772 12: 0781 13: 0782 14: 0791
15: 0792 16: 0800 17: 0801 18: 0802 19: 0803 20: 0804 21: 0805
22: 0806 23: 0807 24: 0808 25: 0809 26: 0810 27: 0811 28: 0812
29: 0813 30: 0814 31: 0815 32: 0816 33: 0817 34: 0818 35: 0819
36: 0820 37: 0821 38: 0822 39: 0823 40: 0824 41: 0825 42: 0826
43: 0827 44: 0828 45: 0829 46: 0830 47: 0831 48: 0832 49: 0833
50: 0834 51: 0835 52: 0836 53: 0837 54: 0838 55: 0839 56: 0840
57: 0841 58: 0842 59: 0843 60: 0844 61: 0845 62: 0846 63: 0847
64: 0848 65: 0849 66: 085 67: 086 68: 087A 69: 087B 70: 088A
71: 088B 72: 089 73: 06000 74: 06001 75: 06002A 76: 06002B
77: 06003A 78: 06003B 79: 06004A 80: 06004B 81: 06005 82: NEMP
83: NEMP8

Statistics: Mean 11.622; Variance 4.271; scale 2.721

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	6513	100.0	6513	66	US-08-554-Sequence 7, Applicatio	0.00e+00
2	6513	100.0	6513	68	US-08-724-Sequence 7, Applicatio	0.00e+00
3	5500	84.4	6519	70	US-08-808-Sequence 24, Applicati	0.00e+00
4	4374	67.2	5461	15	US-07-998-Sequence 7, Applicatio	0.00e+00
5	4374	67.2	5461	15	US-07-998-Sequence 7, Applicatio	0.00e+00
6	3676	56.4	6318	70	US-08-808-Sequence 1, Applicatio	0.00e+00
7	3664	56.3	6315	67	US-08-808-Sequence 2, Applicatio	0.00e+00
8	3662	56.2	6318	67	US-08-608-Sequence 1, Applicatio	0.00e+00

9	3660	56.2	6318	67	US-08-608-Sequence 2, Applicatio	0.00e+00
10	472	7.2	1237	70	US-08-808-Sequence 26, Applicati	0.00e+00
11	320	4.9	6048	67	US-08-682-Sequence 1, Applicatio	0.00e+00
12	312	4.8	3033	49	US-08-334-Sequence 1, Applicatio	0.00e+00
13	298	4.6	6344	66	US-08-511-Sequence 1, Applicatio	6.95e-291
14	296	4.5	6524	69	US-08-775-Sequence 1, Applicatio	1.31e-288
15	296	4.5	6524	67	US-08-669-Sequence 1, Applicatio	1.31e-288
16	296	4.5	6527	67	US-08-669-Sequence 7, Applicatio	1.31e-288
17	296	4.5	6527	69	US-08-775-Sequence 7, Applicatio	1.31e-288
18	296	4.5	7052	69	US-08-775-Sequence 5, Applicatio	1.31e-288
19	296	4.5	7052	67	US-08-669-Sequence 5, Applicatio	1.31e-288
20	231	3.5	2573	67	US-08-669-Sequence 3, Applicatio	4.38e-215
21	231	3.5	2573	69	US-08-775-Sequence 3, Applicatio	4.38e-215
22	214	3.3	930	67	US-08-605-Sequence 2, Applicatio	5.22e-196
23	204	3.1	930	67	US-08-605-Sequence 21, Applicati	7.95e-185
24	194	3.0	930	67	US-08-605-Sequence 3, Applicatio	1.12e-173
25	182	2.9	930	67	US-08-605-Sequence 1, Applicatio	1.89e-171
26	177	2.7	2279	15	US-07-998-Sequence 3, Applicatio	8.41e-155
27	177	2.7	2279	15	US-07-998-Sequence 3, Applicatio	8.41e-155
28	148	2.3	5482	50	US-08-346-Sequence 2, Applicatio	6.65e-123
29	134	2.1	702	66	US-08-511-Sequence 3, Applicatio	1.12e-107
30	119	1.8	5389	50	US-08-346-Sequence 1, Applicatio	1.60e-91
31	110	1.7	7218	39	US-08-232-Sequence 14, Applicati	6.28e-82
32	110	1.7	7218	62	US-08-466-Sequence 14, Applicati	6.28e-82
33	103	1.6	568	15	US-07-998-Sequence 10, Applicati	1.58e-74
34	103	1.6	568	15	US-07-998-Sequence 10, Applicati	1.58e-74
35	95	1.5	578	67	US-08-624-Sequence 14, Applicati	3.83e-66
36	95	1.5	578	66	US-08-569-Sequence 14, Applicati	3.83e-66
37	96	1.5	2416	15	US-07-998-Sequence 1, Applicatio	3.47e-67
38	96	1.5	2416	15	US-07-998-Sequence 1, Applicatio	3.47e-67
39	89	1.4	578	67	US-08-624-Sequence 14, Applicati	6.45e-60
40	89	1.4	578	66	US-08-569-Sequence 14, Applicati	6.45e-60
41	78	1.2	383	60	US-08-446-Sequence 8, Applicatio	1.16e-48
42	78	1.2	383	60	US-08-446-Sequence 8, Applicatio	1.16e-48
43	78	1.2	383	47	US-08-311-Sequence 8, Applicatio	1.16e-48
44	78	1.2	383	60	US-08-446-Sequence 8, Applicatio	1.16e-48
45	78	1.2	383	60	US-08-446-Sequence 8, Applicatio	1.16e-48

ALIGNMENTS

RESULT 1
ID US-08-554-424-7 STANDARD; DNA; UNC; 6513 BP.
AC: xxxxxx
DT: 01-JAN-1900
DE: Sequence 7, Application US/08554424.
CC: Sequence 7, Application US/08554424.
CC: GENERAL INFORMATION:
CC: APPLICANT: Warmke, Jeffrey W.
CC: TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC: TITLE OF INVENTION: PARA SODIUM CHANNEL
CC: NUMBER OF SEQUENCES: 7
CC: CORRESPONDENCE ADDRESS:
CC: ADDRESS: Jack L. Tribble
CC: STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC: CITY: Rahway
CC: STATE: New Jersey
CC: COUNTRY: USA
CC: ZIP: 07065-0907
CC: COMPUTER READABLE FORM:
CC: MEDIUM TYPE: Floppy disk
CC: COMPUTER: IBM PC compatible
CC: OPERATING SYSTEM: PC-DOS/MS-DOS
CC: SOFTWARE: Patent In Release #1.0, Version #1.25
CC: CURRENT APPLICATION DATA:
CC: APPLICATION NUMBER: US/08/554,424
CC: FILING DATE:
CC: CLASSIFICATION: 424
CC: ATTORNEY/AGENT INFORMATION:
CC: NAME: Tribble, Jack L.
CC: REGISTRATION NUMBER: 32,633
CC: REFERENCE/DOCKET NUMBER: 19338DA

Tue Oct 14 14:18:10 1997

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
Sequence 6513 bp; 1681 A; 1548 C; 1702 G; 1582 T; 0 other;

Query Match 100.0%; Score 6513; DB 66; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGACGTTGGCCGATAGACAATGACAGAGATTCGAGTCATATCTGAGGAAGAC 60
QY 1 TCTAGACGTTGGCCGATAGACAATGACAGAGATTCGAGTCATATCTGAGGAAGAC 60
Db 61 GCAGTTGTTCCGTCCTTACCCTGATCATCTGTCGCAATCGAACACGCAATTCGCG 120
QY 61 GCAGTTGTTCCGTCCTTACCCTGATCATCTGTCGCAATCGAACACGCAATTCGCG 120
Db 121 CTGAACATGAAAGCAGAGAGAGCTGGAAGAAAGAGAGCCGAGGAGAGTCCGCGAT 180
QY 121 CTGAACATGAAAGCAGAGAGAGCTGGAAGAAAGAGAGCCGAGGAGAGTCCGCGAT 180
Db 181 ATGCTCGCAAGAAACAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTTC 240
QY 181 ATGCTCGCAAGAAACAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTTC 240
Db 241 CACACCGGATCCCTACACTTGAACAGAGGTGTCGAATACCTGTTGATTCGAGGCGAT 300
QY 241 CACACCGGATCCCTACACTTGAACAGAGGTGTCGAATACCTGTTGATTCGAGGCGAT 300
Db 301 TCCCGCCGGAATGGCTCCTCTCGAGGATATCGATCCTCTACTACAGCAATGTATAC 360
QY 301 TCCCGCCGGAATGGCTCCTCTCGAGGATATCGATCCTCTACTACAGCAATGTATAC 360
Db 361 TGACATTCGTTAGTTAGCAAGAAAGAAATATTTTCGCTTCTGCAATCAAGCAAA 420
QY 361 TGACATTCGTTAGTTAGCAAGAAAGAAATATTTTCGCTTCTGCAATCAAGCAAA 420
Db 421 TGTGGATGCTGATCCATTCGATACGATACGATACGATACGATACGATACGATACG 480
QY 421 TGTGGATGCTGATCCATTCGATACGATACGATACGATACGATACGATACGATACG 480
Db 481 CATTTATTTCCCTATTCATCATCACCACAATTCGTCACATGTCATGATGATATGC 540
QY 481 CATTTATTTCCCTATTCATCATCACCACAATTCGTCACATGTCATGATGATATGC 540
Db 541 CGACACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
QY 541 CGACACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
Db 601 CAGCTGTTAAAGTGATGGCAGCAGGTTTCATTTTATGCCGTTTACGATCTTAGAGATG 660
QY 601 CAGCTGTTAAAGTGATGGCAGCAGGTTTCATTTTATGCCGTTTACGATCTTAGAGATG 660
Db 661 CATGGAATGGCTGGACTTCGTAGTAAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
QY 661 CATGGAATGGCTGGACTTCGTAGTAAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
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QY 721 TAGCTAATCTAGCAGCCCTCGCAACGTTTATAGGTTGTCGAGGCGTTAAACCGTAGCCA 780
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QY 781 TTGTGCCAGGTTTGAAGACCAATCTCGCGCCGCTCATCGAATCGGTGAAGAATCTCGCG 840
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QY 841 ATGTGATATCTGTGACCAATGTTCTCCCTGTGCGTGTTCGCGTGTATGGGCTACAGATCT 900
Db 901 ATATGGCGTGTCTCACCGAGAGATGCAATCAAGAGTTCCTCCGCTGACGAGTTCCTGGGGCA 960
QY 901 ATATGGCGTGTCTCACCGAGAGATGCAATCAAGAGTTCCTCCGCTGACGAGTTCCTGGGGCA 960
Db 961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020
QY 961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020
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QY 1021 ACGAGGCGATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGGCAATCGGACGACG 1080
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QY 1081 ATTACGTTGCTCGAGGGGTTTGGTCCGAATTCGGAATTTATGCTACACGAGTTCGATT 1140
Db 1141 CGTTCCGATGGGCTTTCCTGTCGCGCTTCGCGCTGATGACACAGGACTTCTGGGAGATC 1200
QY 1141 CGTTCCGATGGGCTTTCCTGTCGCGCTTCGCGCTGATGACACAGGACTTCTGGGAGATC 1200
Db 1201 TGTACAGCTGCTGTCGCGCGCGCGGACCATGCGCATGCTGCTTCTTTATAGTATCA 1260
QY 1201 TGTACAGCTGCTGTCGCGCGCGCGGACCATGCGCATGCTGCTTCTTTATAGTATCA 1260
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QY 1261 TCTTCTAGTTCATCTATCTATCTGTAATTTGATTTGGCCATTTGTCCTATGCTGATG 1320
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QY 1321 ACAGATTCGAAAGGAGCGCGGAAGAGAGAGGCTGCGGAAGAGAGAGGCGATAGCTGAAG 1380
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QY 1381 CGGAAGAGCTGCGCGCGCGCGCAAGGCGGCAAGCTGGAGAGGCGGCAATCGCAGGCTC 1440
Db 1441 AGGACAGCGGATGCGGCTGCGCGCGGAGAGAGGCTGCACTGCTCGGAAATGGCCAAAG 1500
QY 1441 AGGACAGCGGATGCGGCTGCGCGCGGAGAGAGGCTGCACTGCTCGGAAATGGCCAAAG 1500
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Db 1561 ACAACAACAAAGAGAGATGTCATTCGAGCGCTCGAGGTGAGTTCGGTGGGCGG 1620
QY 1561 ACAACAACAAAGAGAGATGTCATTCGAGCGCTCGAGGTGAGTTCGGTGGGCGG 1620
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QY 1621 TTATACAAAGACAACACAGCTACACAGCAACAGCTACCAAGTTCTGTAAGTGA 1680
Db 1681 GCACGACATCTTATCTTACCTGTTTCCCGTTTAAACATACGAGGAGTACAGTATGTT 1740
QY 1681 GCACGACATCTTATCTTACCTGTTTCCCGTTTAAACATACGAGGAGTACAGTATGTT 1740
Db 1741 CTCACAAGTACAGTACGAGGAGGAGCGGCTGGCGGTTTGGTATACCCGTTAGCGATCGTA 1800
QY 1741 CTCACAAGTACAGTACGAGGAGGAGCGGCTGGCGGTTTGGTATACCCGTTAGCGATCGTA 1800
Db 1801 AGCCATTTGTTATGTCACATATCAGGATGCGCAGCAGCTTGCCTTATGCCGACGACT 1860
QY 1801 AGCCATTTGTTATGTCACATATCAGGATGCGCAGCAGCTTGCCTTATGCCGACGACT 1860
Db 1861 CGAATGCGCTCAACCCGCGATGTCGGAAGAGAAATGGGCGCATCATAGTCCCGTGTACTATG 1920
QY 1861 CGAATGCGCTCAACCCGCGATGTCGGAAGAGAAATGGGCGCATCATAGTCCCGTGTACTATG 1920
Db 1921 GCAATCTAGGCTCCGACACTCATCTATACCTTCGATCAGTCCCGCAATATCGTATACCT 1980
QY 1921 GCAATCTAGGCTCCGACACTCATCTATACCTTCGATCAGTCCCGCAATATCGTATACCT 1980

QY 1921 GCAATCTAGGCTCCGACACTCATCGTATACCTCGCATCAGTCCGGAATATCGTATACCT 1980
Db 1981 CACATGGCATCTACTCGCGGCGATGGCGTCTATGGCGTCAAGCAATGACCAAGGAGA 2040
QY 1981 CACATGGCATCTACTCGCGGCGATGGCGTCTATGGCGTCAAGCAATGACCAAGGAGA 2040
Db 2041 GCAAAATGGCAACCGCAACACACGCAATCAATCAGTGGCGCCACCAATGGCGGACCA 2100
QY 2041 GCAAAATGGCAACCGCAACACACGCAATCAATCAGTGGCGCCACCAATGGCGGACCA 2100
Db 2101 CCGTCTGGACACCAATCAAGCTCGATCATCGGACCTACGAAATTTGGCCTGGAGTGA 2160
QY 2101 CCGTCTGGACACCAATCAAGCTCGATCATCGGACCTACGAAATTTGGCCTGGAGTGA 2160
Db 2161 CGGACCAAGCTGCGAGATTAACATCATGACAACTCTTTTATCGAGCCCGTCCAGACAC 2220
QY 2161 CGGACCAAGCTGCGAGATTAACATCATGACAACTCTTTTATCGAGCCCGTCCAGACAC 2220
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QY 2221 AAACGGTGGTTGATATGAAGATGTGATGCTCCTGAATGACATCATCGAACAGGCGGCTG 2280
Db 2281 GTCCGACAGTGGGCAAGCGATCGGGTGTCTCCGTTTACTATTTCCCAACAGAGGAGC 2340
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QY 2341 ATGACGAGATGGGCGAGCTTCAAGACAAAGCACTCGAAGTGATCTCAAGGCGATCG 2400
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QY 2701 CGCTATTGGAACCTGGGACTCGAGGGTGTCCAGGGTCTGTCGGTATTGCGGTTCTTTTCGAT 2760
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QY 2881 TCCTTCGGTGTATGGGAATGCAACTGTTCGGAAGAAATATCATATGATCAAGGACCGGT 2940
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QY 3001 TGTTCGGGTCCTCGGGAATGATGAGTCCATGTGGGACTGCATGTAGTGGGG 3060

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QY 3121 ACCTTTTCTTAGCCTTGTGTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCGACTG 3180
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Db 3241 GGGTTAAGCGTAATATGCTGATTTTCAAGTTAATACGTAACAAATGACAAATCAAA 3300
QY 3241 GGGTTAAGCGTAATATGCTGATTTTCAAGTTAATACGTAACAAATGACAAATCAAA 3300
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QY 3301 TAAAGTATCAACCATCAGGTGAGAGCAACAGATCAGTTGGATTTGGAGCGAAGAGC 3360
Db 3361 ATGGTGTACAACGAATGAGCTGGGCGCCAGCAGAGATCCTCGCCGACGCGCTCATCAAG 3420
QY 3361 ATGGTGTACAACGAATGAGCTGGGCGCCAGCAGAGATCCTCGCCGACGCGCTCATCAAG 3420
Db 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGATCGGATGGAATTCACGA 3480
QY 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGATCGGATGGAATTCACGA 3480
Db 3481 TACACGGGACATGAAGAACAAACAGCGAAGAAATCCAAATATCTAAATACGCAACGA 3540
QY 3481 TACACGGGACATGAAGAACAAACAGCGAAGAAATCCAAATATCTAAATACGCAACGA 3540
Db 3541 TGATTTGGCAACTCAATTAACCAAGCAATAGACTGGAACACGACTAAACCATAGAG 3600
QY 3541 TGATTTGGCAACTCAATTAACCAAGCAATAGACTGGAACACGACTAAACCATAGAG 3600
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QY 3601 GTTTGTCTTTACAGGACGACACTGCGCAGCATTAATCTATGTTAGTCCATTAAGAATC 3660
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QY 3661 GACCATTAAGGACGAGAGCCACAAGGGAGCGCCGAGACGATGGAGGCGAGAGAGC 3720
Db 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGAGAGGAACTGACGAGGAGGCGGAATGCG 3780
QY 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGAGAGGAACTGACGAGGAGGCGGAATGCG 3780
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QY 3781 AGGAGGCGCGCTCGACGGTGATATCATTTATCATGACACGACGAGGATATCTCGATG 3840
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QY 3841 AATATCCAGCTGATTTGCTCCCGGATTCGTACTATAAGAAATTTCCGATTTAGCGGGT 3900
Db 3901 ACGATCACTCGCGCTTCTGGCAAGGATGGGCAATTTAGGACTGAAACTTTTCAATTAA 3960
QY 3901 ACGATCACTCGCGCTTCTGGCAAGGATGGGCAATTTAGGACTGAAACTTTTCAATTAA 3960
Db 3961 TTGAAATAAATATTTTGAACAGCTGTTATCACTATGATTTTAAATGACTAGCTTAGCTT 4020
QY 3961 TTGAAATAAATATTTTGAACAGCTGTTATCACTATGATTTTAAATGACTAGCTTAGCTT 4020
Db 4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATCTCGAGGATTTTATCTATA 4080
QY 4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATCTCGAGGATTTTATCTATA 4080
Db 4081 TGGACAGATATTTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTTGGGCTCG 4140
QY 4081 TGGACAGATATTTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTTGGGCTCG 4140

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Db 6361 CGCGCGTTCCTGTTGAGAGCAGCGGTTCTGTCACGAAGACGCCACAGGTGGTCAATCC 6420
QY 6361 CGCGCGTTCCTGTTGAGAGCAGCGGTTCTGTCACGAAGACGCCACAGGTGGTCAATCC 6420
Db 6421 ACTCGGATCGCGGAGCATCAGTCGCGCACGCGCGGATGTCCTGAGCAGGCGCTCGCCCCC 6480
QY 6421 ACTCGGATCGCGGAGCATCAGTCGCGCACGCGCGGATGTCCTGAGCAGGCGCTCGCCCCC 6480
Db 6481 CCTTCAAGATCAGCGGAGTATTAGCTCTAGA 6513
QY 6481 CCTTCAAGATCAGCGGAGTATTAGCTCTAGA 6513

RESULT 2
ID US-08-724-095-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 7, Application US/08724095.
CC Sequence 7, Application US/08724095
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Hall, Linda
CC APPLICANT: Feng, Gouping
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
CC STREET: P.O. Box 2000 - 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTseq Version #1.05
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/724,095
CC FILING DATE:
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hand, J. Mark
CC REGISTRATION NUMBER: 36,545
CC REFERENCE/DOCKET NUMBER: 19332DA
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6513 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 other;

Query Match 100.0%; Score 6513; DB 68; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGAGTTGGCGGATAGACAATGACAGAGATCCGACTCGATATCTGAGGAAGAAC 60
QY 1 TCTAGAGTTGGCGGATAGACAATGACAGAGATCCGACTCGATATCTGAGGAAGAAC 60
Db 61 GCAGTTGTTCCGTCCTTACCGGATCATTTGGTGCAATCGAATCGAACAACGATTCGG 120
QY 61 GCAGTTGTTCCGTCCTTACCGGATCATTTGGTGCAATCGAATCGAACAACGATTCGG 120

Db 121 CTGAACATGAAAGCAGAGGAGCTGGAAGAAAGAGAGCCGAGGAGGTGCCCGCAT 180
QY 121 CTGAACATGAAAGCAGAGGAGCTGGAAGAAAGAGAGCCGAGGAGGTGCCCGCAT 180
Db 181 ATGGTCCGAAGAAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTTC 240
QY 181 ATGGTCCGAAGAAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTTC 240
Db 241 CACACCCGATCCTACCTTGACAGGGGTGCGCCAAATACCTGTTGATGTCAGGCGAGCT 300
QY 241 CACACCCGATCCTACCTTGACAGGGGTGCGCCAAATACCTGTTGATGTCAGGCGAGCT 300
Db 301 TCCCGCCGGAATTTGGCCTCCACTCTCTCGAGGATATCGATCCCTACTACACCAATGTAC 360
QY 301 TCCCGCCGGAATTTGGCCTCCACTCTCTCGAGGATATCGATCCCTACTACACCAATGTAC 360
Db 361 TGACATTCGTAGTTGTAAGCAAGAAAAAGATATTTTTCGCTTTTCTGCTGATCAAAAGCA 420
QY 361 TGACATTCGTAGTTGTAAGCAAGAAAAAGATATTTTTCGCTTTTCTGCTGATCAAAAGCA 420
Db 421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTTCTAGTGCATC 480
QY 421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTTCTAGTGCATC 480
Db 481 CATTAATTTTCCCTATTCATCATCACCAATCTCTCAACTGCATCTCTGATGATAATGC 540
QY 481 CATTAATTTTCCCTATTCATCATCACCAATCTCTCAACTGCATCTCTGATGATAATGC 540
Db 541 CGACAACGCCACGCTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
QY 541 CGACAACGCCACGCTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
Db 601 CAGCTGTTAAAGTGATGGCAGAGGTTTCATTTATGTCGCGTTTACGTATCTTAGAGATG 660
QY 601 CAGCTGTTAAAGTGATGGCAGAGGTTTCATTTATGTCGCGTTTACGTATCTTAGAGATG 660
Db 661 CATGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
QY 661 CATGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
Db 721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTCTCGGAGCGCTTAAACCCGTAGCCA 780
QY 721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTCTCGGAGCGCTTAAACCCGTAGCCA 780
Db 781 TTGTCCAGGCTTGAAGACCATCTGCGCGCTCATCGAATCGGTGAAGATCTGCGCG 840
QY 781 TTGTCCAGGCTTGAAGACCATCTGCGCGCGCTCATCGAATCGGTGAAGATCTGCGCG 840
Db 841 ATGTGATTATCCTGACCATGTTTCTCCCTGTGCGGTGTTGCGGTTGATGGGCTTACAGATCT 900
QY 841 ATGTGATTATCCTGACCATGTTTCTCCCTGTGCGGTGTTGCGGTTGATGGGCTTACAGATCT 900
Db 901 ATATGGCGGTGCTCACCAGAGAGTGCATCAAGAAGTTTCCCGCTGACGCGTTCTGGGCA 960
QY 901 ATATGGCGGTGCTCACCAGAGAGTGCATCAAGAAGTTTCCCGCTGACGCGTTCTGGGCA 960
Db 961 ATCTGACCGACGAGAACTGGGACTATCAATCGCAATAGCTCCAAATGGTATTCGGAGG 1020
QY 961 ATCTGACCGACGAGAACTGGGACTATCAATCGCAATAGCTCCAAATGGTATTCGGAGG 1020
Db 1021 ACGAGGATCTCATTTCCGTTATCGGCAATATATCCGGTTCGGGGCAATCGCAGCAGC 1080
QY 1021 ACGAGGATCTCATTTCCGTTATCGGCAATATATCCGGTTCGGGGCAATCGCAGCAGC 1080
Db 1081 ATTAGCTGCTCGCAGGGGTTGGTCCGAATCCGAATATGGCTTACACCAGCTTCGATT 1140
QY 1081 ATTAGCTGCTCGCAGGGGTTGGTCCGAATCCGAATATGGCTTACACCAGCTTCGATT 1140
Db 1141 CGTTCGGATGGCTTTCCTGTCGCGCTTCCCGCTGATGACACAGGACTTCTGGGAGGATC 1200
QY 1141 CGTTCGGATGGCTTTCCTGTCGCGCTTCCCGCTGATGACACAGGACTTCTGGGAGGATC 1200
Db 1201 TGTACCAGCTGGTGTGGCGCGCCCGGACCATGTCATGCTGTTTATAGTCAATCA 1260

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QY	1201	TGTTACAGCTGGTGTGCGCGCGCGGACCATGGGCACATGCTGTCTTTATAGTCATCA	1260
Db	1261	TCTTCTAGGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATGTCGTATG	1320
QY	1261	TCTTCTAGGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATGTCGTATG	1320
Db	1321	ACGAATTCGAAGGAAGCGCGAAGAAGAGGCTGCCGAAGAGGAGGATACGTGAAG	1380
QY	1321	ACGAATTCGAAGGAAGCGCGAAGAAGAGGCTGCCGAAGAGGAGGATACGTGAAG	1380
Db	1381	CGGAAGAAGCTGCCGCGCGCGAAGCGCGAAGAGGCTGCCGAAGAGGAGGATACGTGAAG	1440
QY	1381	CGGAAGAAGCTGCCGCGCGCGAAGCGCGAAGAGGCTGCCGAAGAGGAGGATACGTGAAG	1440
Db	1441	AGCGAGCAGCGGATCGCGCTGCCGCGAAGAGGCTGCCGAAGAGGAGGATACGTGAAG	1500
QY	1441	AGCGAGCAGCGGATCGCGCTGCCGCGAAGAGGCTGCCGAAGAGGAGGATACGTGAAG	1500
Db	1501	GTCCGAGCTATCTTGCATCAGCTATGAGCTATTGTTGGCGGCGAGAAGGCGCAACGATG	1560
QY	1501	GTCCGAGCTATCTTGCATCAGCTATGAGCTATTGTTGGCGGCGAGAAGGCGCAACGATG	1560
Db	1561	ACAACAACAAGAGAAGATGTCATTCGAGAGCGTCGAGGTGAGTCGAGGTGCGTGAGCG	1620
QY	1561	ACAACAACAAGAGAAGATGTCATTCGAGAGCGTCGAGGTGAGTCGAGGTGCGTGAGCG	1620
Db	1621	TTATACAAGAGAACAGCAGCTACCAACAGCACACCAAGCTACCAAAAGTTCGTAAGTGA	1680
QY	1621	TTATACAAGAGAACAGCAGCTACCAACAGCACACCAAGCTACCAAAAGTTCGTAAGTGA	1680
Db	1681	GCAGCAGCTCTTATCTTACCTTGGTTTACCGGTTTAAACATACGAGGAGGATCAGTAGTT	1740
QY	1681	GCAGCAGCTCTTATCTTACCTTGGTTTACCGGTTTAAACATACGAGGAGGATCAGTAGTT	1740
Db	1741	CTCACAAGTACAGATACGAGGAGGAGGCGGCGCTTTGGTATACCGGCTAGCGATCGTA	1800
QY	1741	CTCACAAGTACAGATACGAGGAGGAGGCGGCGCTTTGGTATACCGGCTAGCGATCGTA	1800
Db	1801	AGCCATTGGTATTGTCAACATATCAGATGCCAGAGCAGCTTGGCCCTATGCGGAGCT	1860
QY	1801	AGCCATTGGTATTGTCAACATATCAGATGCCAGAGCAGCTTGGCCCTATGCGGAGCT	1860
Db	1861	CGAATGCCGTCAACCGGATGTCGAAGAGATGGGCGCATCATAGTGGCCGCTGACTATG	1920
QY	1861	CGAATGCCGTCAACCGGATGTCGAAGAGATGGGCGCATCATAGTGGCCGCTGACTATG	1920
Db	1921	GCAATCTAGGCTCCGACACTCATCGTATACCTCGCATGTCGCGAATATCGTATACCT	1980
QY	1921	GCAATCTAGGCTCCGACACTCATCGTATACCTCGCATGTCGCGAATATCGTATACCT	1980
Db	1981	CACATGGGATATCTCGGCGCATGGCGGTCATGGCGTCAGCACCAATGACCAAGGAGA	2040
QY	1981	CACATGGGATATCTCGGCGCATGGCGGTCATGGCGTCAGCACCAATGACCAAGGAGA	2040
Db	2041	GCAAAATGCGCAACCGCACACACCAATCATAGTGGGCGCCACCAATGGCGGACCA	2100
QY	2041	GCAAAATGCGCAACCGCACACACCAATCATAGTGGGCGCCACCAATGGCGGACCA	2100
Db	2101	CCTGTCTGGACACCAATCATAGCTCGATCATCGGCTACGAAATGGCGCTGGAGTGA	2160
QY	2101	CCTGTCTGGACACCAATCATAGCTCGATCATCGGCTACGAAATGGCGCTGGAGTGA	2160
Db	2161	CGGACGAAGCTGCAAGATTAACATCATGACAACTCTTTATCGAGCCGCTCCAGACAC	2220
QY	2161	CGGACGAAGCTGCAAGATTAACATCATGACAACTCTTTATCGAGCCGCTCCAGACAC	2220
Db	2221	AAACGGTGGTATGATGAAGATGATGCTGCTGATGACATCATCGAACAGGCGCGTG	2280
QY	2221	AAACGGTGGTATGATGAAGATGATGCTGCTGATGACATCATCGAACAGGCGCGTG	2280
Db	2281	GTCCGCAAGTCGCGGCAAGGATCGCGGTGCTCCGTTTACTATTTCCTCCACAGAGGAGC	2340
QY	2281	GTCCGCAAGTCGCGGCAAGGATCGCGGTGCTCCGTTTACTATTTCCTCCACAGAGGAGC	2340
Db	2341	ATGACGAGGATGGCGGACAGCTTCAAGACAGGCACTCGAAGTGTATCTCAAGGCACTCG	2400
QY	2341	ATGACGAGGATGGCGGACAGCTTCAAGACAGGCACTCGAAGTGTATCTCAAGGCACTCG	2400
Db	2401	ATGTTGTTTGTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATGCG	2460
QY	2401	ATGTTGTTTGTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATGCG	2460
Db	2461	TCATCGTCTTCGATCCCTTCGTCAGGCTTTCATCAGCGCTGTCATGTTGGTCAACACGA	2520
QY	2461	TCATCGTCTTCGATCCCTTCGTCAGGCTTTCATCAGCGCTGTCATGTTGGTCAACACGA	2520
Db	2521	TGTTTCATGCGCAATGGATACCCACGATATGAACAAGAGATGGAACGCGTCTCAAGAGTG	2580
QY	2521	TGTTTCATGCGCAATGGATACCCACGATATGAACAAGAGATGGAACGCGTCTCAAGAGTG	2580
Db	2581	GCAACTATTTCTTCCAGCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA	2640
QY	2581	GCAACTATTTCTTCCAGCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA	2640
Db	2641	GCCCCAAGTACTATTTCAGGAGGCTGGAAACATCTTCGACTTCATTCATTCGTCGCTAT	2700
QY	2641	GCCCCAAGTACTATTTCAGGAGGCTGGAAACATCTTCGACTTCATTCATTCGTCGCTAT	2700
Db	2701	CGCTATTGGAACCTGGGACTCGAGGCTGTCAGGCTGTCGCGTATTCGCTTCCTTCGAT	2760
QY	2701	CGCTATTGGAACCTGGGACTCGAGGCTGTCAGGCTGTCGCGTATTCGCTTCCTTCGAT	2760
Db	2761	TGTGCGGTATTCAACTGGCCAAAGTCTTGGCCCACTTTAAATTTACTTCATTCGATTA	2820
QY	2761	TGTGCGGTATTCAACTGGCCAAAGTCTTGGCCCACTTTAAATTTACTTCATTCGATTA	2820
Db	2821	TGGGACGACCATGGGCGCTTTGGGTAACTGACATTTGTTACTTTGCAATATCATCTTCA	2880
QY	2821	TGGGACGACCATGGGCGCTTTGGGTAACTGACATTTGTTACTTTGCAATATCATCTTCA	2880
Db	2881	TCCTTGGGATGGGAAATGCAACTGTCGGAAGAAATATCATGATCACAAGGACCGCT	2940
QY	2881	TCCTTGGGATGGGAAATGCAACTGTCGGAAGAAATATCATGATCACAAGGACCGCT	2940
Db	2941	TTCCGGATGGCGACTTCCCGCGCTGGAACCTTCCAGGCTTTATGCAAGCTTCATGATCG	3000
QY	2941	TTCCGGATGGCGACTTCCCGCGCTGGAACCTTCCAGGCTTTATGCAAGCTTCATGATCG	3000
Db	3001	TGTTCCGGGTGCTCTGGGAGATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG	3060
QY	3001	TGTTCCGGGTGCTCTGGGAGATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG	3060
Db	3061	ATGTCCTGTCATTCCTTCTTGGCCACCGTGTGTCGCAATCTTGTGGTACTTAA	3120
QY	3061	ATGTCCTGTCATTCCTTCTTGGCCACCGTGTGTCGCAATCTTGTGGTACTTAA	3120
Db	3121	ACCTTTCTTAGCTTGTGTTTGGTTCATCTAGCTTATCAGCCCGACTG	3180
QY	3121	ACCTTTCTTAGCTTGTGTTTGGTTCATCTAGCTTATCAGCCCGACTG	3180
Db	3181	CCGATAACGATACGAATATAATAGCCAGGCTTCAATCGAATTTGGCCGATTTAAAGTT	3240
QY	3181	CCGATAACGATACGAATATAATAGCCAGGCTTCAATCGAATTTGGCCGATTTAAAGTT	3240
Db	3241	GGGTTAAGCGTAAATGCTGATTTTCAAGTTAATACGTAACAAATTTGACAAATCAAA	3300
QY	3241	GGGTTAAGCGTAAATGCTGATTTTCAAGTTAATACGTAACAAATTTGACAAATCAAA	3300
Db	3301	TAAGTGATCAACCATCAGGTGAGAGCAACACAGATCAGTTGGATTTGGAGCGAAGAGC	3360
QY	3301	TAAGTGATCAACCATCAGGTGAGAGCAACACAGATCAGTTGGATTTGGAGCGAAGAGC	3360
Db	3361	ATGGTGACAAAGCTGGGCTGGCGCAGGAGATCTCCGCCGACGCGCTTCATCAAGA	3420
QY	3361	ATGGTGACAAAGCTGGGCTGGCGCAGGAGATCTCCGCCGACGCGCTTCATCAAGA	3420

Db 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGGTGCCCATCGGGATCGGATGGAATTCACGA 3480
Qy |||||
Db 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGGTGCCCATCGGGATCGGATGGAATTCACGA 3480
Qy |||||
Db 3481 TACACGGGCACATGAAGAACACAAAGCCGAGAGAAATCCAAATATCTAAATAACGCAAGA 3540
Qy |||||
Db 3481 TACACGGGCACATGAAGAACACAAAGCCGAGAGAAATCCAAATATCTAAATAACGCAAGA 3540
Qy |||||
Db 3541 TGAATGGCAACTCAATTAACCAACCAAGACAATAGACTGGAACACAGACTAAACCATAGAG 3600
Qy |||||
Db 3541 TGAATGGCAACTCAATTAACCAACCAAGACAATAGACTGGAACACAGACTAAACCATAGAG 3600
Qy |||||
Db 3601 GTTTGTCTTACAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCCAATAAGATC 3660
Qy |||||
Db 3601 GTTTGTCTTACAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCCAATAAGATC 3660
Qy |||||
Db 3661 GACCATTCAAGGACGAGAGCCACAAGGGCAGCGCGAGACGATGAGGGCGAGGAGAAAGC 3720
Qy |||||
Db 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGAGGCGGAATGCG 3780
Qy |||||
Db 3721 GCGAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGAGGCGGAATGCG 3780
Qy |||||
Db 3781 AGGAGGGCCGCTCGACGGTGATATCATTTATTCATGCACACGAGGATATACCTCGATG 3840
Qy |||||
Db 3781 AGGAGGGCCGCTCGACGGTGATATCATTTATTCATGCACACGAGGATATACCTCGATG 3840
Qy |||||
Db 3841 AATATCCAGCTGATGTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTTAGCCGGTG 3900
Qy |||||
Db 3901 ACGATGACTCGCGGTCTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Qy |||||
Db 3961 TTGAAATAAATATTTGAAACAGCTGTTATCACTATGATTTAATAGTAGCTTAGCTT 4020
Qy |||||
Db 4021 TGGCAATTAGAAGATGTACATCTGCCACAAGACCCATACCTGAGGATATTTATACATA 4080
Qy |||||
Db 4081 TGGCAGAAATATTACGGTTATATCTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Qy |||||
Db 4141 GCTTCAAAGTGACTTCAACACGCGTGTGTGGCTCGATTTCGTGATGTGATGGTAT 4200
Qy |||||
Db 4201 CGCTTATCAACTCGTGTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
Qy |||||
Db 4261 TCGGAACGTTAAGAGCAGCTGAGACCACTACGTGCCATGTCCTGATGCAAGGCGATGAGG 4320
Qy |||||
Db 4321 TCGTGTAAATCGCTGTGTACAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGTC 4380
Qy |||||
Db 4381 TAAATTTTGGCTAATTTTGGCAATAATGGGTGTACAGCTTTTGGTGGAAATATTTTA 4440
Qy |||||
Db 4441 AGTGGAGGACATGATGSCACGAGCTCAGCCAGGAGATCATACCAATCGCAATGCCT 4500
Qy |||||
Db 4441 AGTGGAGGACATGATGSCACGAGCTCAGCCAGGAGATCATACCAATCGCAATGCCT 4500

Db 4501 GCGAGAGCAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAAACG 4560
Qy |||||
Db 4501 GCGAGAGCAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAAACG 4560
Qy |||||
Db 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAGAGCTGGATACAAATCATGAACGATG 4620
Qy |||||
Db 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAGAGCTGGATACAAATCATGAACGATG 4620
Qy |||||
Db 4621 CTATCGATTACGAGAGGTGGACAAAGCAATTCGTGAAACGAACATCTACATGTATT 4680
Qy |||||
Db 4621 CTATCGATTACGAGAGGTGGACAAAGCAATTCGTGAAACGAACATCTACATGTATT 4680
Qy |||||
Db 4681 TATATTTCTTCTTCTCATATTTGGATCCTTTTTCACACTCAATCTGTTTCAATGGTG 4740
Qy |||||
Db 4681 TATATTTCTTCTTCTCATATTTGGATCCTTTTTCACACTCAATCTGTTTCAATGGTG 4740
Qy |||||
Db 4741 TTATCATTTGATAATTTTATGAGCAAAAAGAAAAGAGAGTGGATCATAGNAATGTTCA 4800
Qy |||||
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Qy |||||
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Qy |||||
Db 4861 TAAAGCCATTCCRAAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAAACG 4920
Qy |||||
Db 4861 TAAAGCCATTCCRAAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAAACG 4920
Qy |||||
Db 4921 ATAAGAAATTCGATATAATCATATTATGTTTATTCATTGGTCTGNAACATGTTACCATGACCC 4980
Qy |||||
Db 4921 ATAAGAAATTCGATATAATCATATTATGTTTATTCATTGGTCTGNAACATGTTACCATGACCC 4980
Qy |||||
Db 4981 TCGATGCTTACGATCGCTGGACACGATATAACGGGTCTTAGACTATCTCAATGGGAT 5040
Qy |||||
Db 4981 TCGATGCTTACGATCGCTGGACACGATATAACGGGTCTTAGACTATCTCAATGGGAT 5040
Qy |||||
Db 5041 TCGTATGTTATTTTTCAGTTCGGAATGCTATTAAATAATTTTCGTTTACGATATCACTATT 5100
Qy |||||
Db 5041 TCGTATGTTATTTTTCAGTTCGGAATGCTATTAAATAATTTTCGTTTACGATATCACTATT 5100
Qy |||||
Db 5101 TTATTTAGCCATGGAATTTATTTGATGATGATGTTGATGTTTATTTATTTATTTTATTTT 5160
Qy |||||
Db 5161 TACTTTAGCGATATTATCGAAGATGTTTCTGCTGCCACACCTCTCGAGTGGTGGCTG 5220
Qy |||||
Db 5161 TACTTTAGCGATATTATCGAAGATGTTTCTGCTGCCACACCTCTCGAGTGGTGGCTG 5220
Qy |||||
Db 5221 TGGCGAAAGTGGCGGTGTCTTCGACTGGTGAAGGGAGCCAAAGGGCATTCGGACACTGC 5280
Qy |||||
Db 5221 TGGCGAAAGTGGCGGTGTCTTCGACTGGTGAAGGGAGCCAAAGGGCATTCGGACACTGC 5280
Qy |||||
Db 5281 TCTTCGCTTGGCCATGTCGCTGCCGCGCTGTTCAACATCTGCTGCTGCTGCTGCTG 5340
Qy |||||
Db 5281 TCTTCGCTTGGCCATGTCGCTGCCGCGCTGTTCAACATCTGCTGCTGCTGCTGCTG 5340
Qy |||||
Db 5341 TCATCTTCTATCTTTGCCATTTTCGGCATGTCGTTCTTCTCATGCACGTGAAGGAGAGAGCG 5400
Qy |||||
Db 5341 TCATCTTCTATCTTTGCCATTTTCGGCATGTCGTTCTTCTCATGCACGTGAAGGAGAGAGCG 5400
Qy |||||
Db 5401 GCATTAACGAGCTCTACAACTTTCAAGAGCTTTGGCCAGAGCATGATCTGCTCTTTTCA 5460
Qy |||||
Db 5461 TGTCTACCTCAGCCGTTGGGATGGTGTACTGGAGCCCATTTCAATGAGGAGAGCATGCG 5520
Qy |||||
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Qy |||||
Db 5521 ATCCACCCGAGACGACAAAGGCTATCCGGCAATTTGGTTCAGGACCGTTTGAATAA 5580
Qy |||||
Db 5521 ATCCACCCGAGACGACAAAGGCTATCCGGCAATTTGGTTCAGGACCGTTTGAATAA 5580
Qy |||||
Db 5581 CGTTTCTCTCTCATACCTAGTTATAAGCTTTTGTATAGTTATTATATATGATACATTGCTG 5640

QY 384 GGAAGAATATTTTCGCTTTTTCGATCAAAAGCAATGTGGATGCTCGATTCATTCAT 443
Db 421 CGGATACGTCGTGCGCCATTTACATTTCTAGTGCATCATATTTTCCCTTATTCATATC 480
QY 444 CGGATACGTCGTGCGCCATTTACATTTCTAGTGCATCATATTTTCCCTTATTCATATC 503
Db 481 ACCCAATTCGCTGCACTGCACTGATGATAAATCGCGACAACGCCACGGTTGAGTCC 540
QY 504 ACCCAATTCGCTGCACTGCACTGATGATAAATCGCGACAACGCCACGGTTGAGTCC 563
Db 541 ACTGAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGAATGCGACA 600
QY 564 ACTGAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGAATGCGACA 623
Db 601 GGTTCATTTATGCGCGTTTACGATCTTAGAGATGATGAATGGCTGGACATTCGTA 660
QY 624 GGTTCATTTATGCGCGTTTACGATCTTAGAGATGATGAATGGCTGGACATTCGTA 683
Db 661 GTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATTTAGTGAATCTAGCAGCCCTGCGA 720
QY 684 GTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATTTAGTGAATCTAGCAGCCCTGCGA 743
Db 721 AGCTTTAGGTGCTCGGAGCGTTTAAACCGTAGCCATGTGCCAGGCTTGAAGACATC 780
QY 744 AGCTTTAGGTGCTCGGAGCGTTTAAACCGTAGCCATGTGCCAGGCTTGAAGACATC 803
Db 781 GTCGCGCGCTCATCGAATCGGTGAAGATCTGCCGATGTGATTATCTGACCATGTTTC 840
QY 804 GTCGCGCGCTCATCGAATCGGTGAAGATCTGCCGATGTGATTATCTGACCATGTTTC 863
Db 841 TCCCTGTCGGTGTTCGCGTTGATGGCCCTACAGATCTATATGGGCGTGTCCACCGAGAAG 900
QY 864 TCCCTGTCGGTGTTCGCGTTGATGGCCCTACAGATCTATATGGGCGTGTCCACCGAGAAG 923
Db 901 TGCATCAAGAGTTCCGCTGACAGCGTTCTCGGGCAATCTGACCGAGAGAACTGGGAC 960
QY 924 TGCATCAAGAGTTCCGCTGACAGCGTTCTCGGGCAATCTGACCGAGAGAACTGGGAC 983
Db 961 TATCAATCGCAATAGCTCCAAATGGTATCCGAGGAGGAGGATCTCATTTCCGTTA 1020
QY 984 TATCAATCGCAATAGCTCCAAATGGTATCCGAGGAGGAGGATCTCATTTCCGTTA 1043
Db 1021 TCGCGCAATATATCGGTCGCGGGCAATCGACACGATACGTTGCTGCGAGGGGTTT 1080
QY 1044 TCGCGCAATATATCGGTCGCGGGCAATCGACACGATACGTTGCTGCGAGGGGTTT 1103
Db 1081 GGTCCGAATCCGAATATGGCTACACAGCTTCGATTCGGATGGCTTCTGTGCC 1140
QY 1104 GGTCCGAATCCGAATATGGCTACACAGCTTCGATTCGGATGGCTTCTGTGCC 1163
Db 1141 GCCTTCCGCTGATGACACAGACTTCTGGGAGGATCTGTACAGCTGGTGTGGCGGC 1200
QY 1164 GCCTTCCGCTGATGACACAGACTTCTGGGAGGATCTGTACAGCTGGTGTGGCGGC 1223
Db 1201 GCCGACCATGACATGCTGTTCTTTATAGTCAATCTTCTAGGTTCAATTCATCTT 1260
QY 1224 GCCGACCATGACATGCTGTTCTTTATAGTCAATCTTCTAGGTTCAATTCATCTT 1283
Db 1261 GTGAATTTGATTTTGGCCATTTGTCATGCTGTATGACGAATTCGAAGAGGAGCCGNA 1320
QY 1284 GTGAATTTGATTTTGGCCATTTGTCATGCTGTATGACGAATTCGAAGAGGAGCCGNA 1343
Db 1321 GAAGAAGAGGCTCGCGAAGAGGAGCGATACGTTGAAGCGGAAGAGCTGCCGCCGCCAAA 1380
QY 1344 GAAGAAGAGGCTCGCGAAGAGGAGCGGATACGTTGAAGCGGAAGAGCTGCCGCCGCCAAA 1403
Db 1381 GCGGCCAAGCTGAGGAGCGGCCAATGCGAGGCTCAGGACAGCGGATCGGCTGCC 1440
QY 1404 GCGGCCAAGCTGAGGAGCGGCCAATGCGAGGCTCAGGACAGCGGATCGGCTGCC 1463
Db 1441 GCGGAAGAGGCTGCACTGATCCGGAATGGCCAGAGTCCGACGATTTCTTGCATCAGC 1500
QY 1464 GCGGAAGAGGCTGCACTGATCCGGAATGGCCAGAGTCCGACGATTTCTTGCATCAGC 1523

Db 1501 TATGAGCTATTTTGGCGGAGAGGGCAACGATGACAACAACAAGAGAAGATGTCC 1560
QY 1524 TATGAGCTATTTTGGCGGAGAGAGGGCAACGATGACAACAACAAGAGAAGATGTCC 1583
Db 1561 ATTGCGAGCGTCGAGGTGGAGTCGGAGTCGGTAGCGTTTATACAAAGACAACCGACACT 1620
QY 1584 ATTGCGAGCGTCGAGGTGGAGTCGGAGTCGGTAGCGTTTATACAAAGACAACCGACACT 1643
Db 1621 ACCACAGCACACCAAGCTTACCAAGTTCTGTAAGTGACGACGACATCTTATCTTACT 1680
QY 1644 ACCACAGCACACCAAGCTTACCAAGTTCTGTAAGTGACGACGACATCTTATCTTACT 1703
Db 1681 GGTTCACCGTTTAAACATACGACAGGGATCAGTGTCTCACAAGTACACGATACGGAAAC 1740
QY 1704 GGTTCACCGTTTAAACATACGACAGGGATCAGTGTCTCACAAGTACACGATACGGAAAC 1763
Db 1741 GGAGTGGCCGCTTTGGTATACCCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATAT 1800
QY 1764 GGAGTGGCCGCTTTGGTATACCCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATAT 1823
Db 1801 CAGGATGCCAGCAGCACTTGCCTTATGCCGACGACTCGAATGCCGTCAACCCGATGTCC 1860
QY 1824 CAGGATGCCAGCAGCACTTGCCTTATGCCGACGACTCGAATGCCGTCAACCCGATGTCC 1883
Db 1861 GAAGAGAATGGGCGCATCATAGTGCCTGTACTATATGGCAATCTAGGCTCCGACACTCA 1920
QY 1884 GAAGAGAATGGGCGCATCATAGTGCCTGTACTATATGGCAATCTAGGCTCCGACACTCA 1943
Db 1921 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGCGGC 1980
QY 1944 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGCGGC 2003
Db 1981 ATGCCGCTCATGGGCGTCAGCACATGACCAAGAGAGACAAATTCGCAACCGCAACACA 2040
QY 2004 ATGCCGCTCATGGGCGTCAGCACATGACCAAGAGAGACAAATTCGCAACCGCAACACA 2063
Db 2041 CGCAATCAATCAGTGGGCGCCACCAATGGCGCACCACTGTCTGGACACCAATCACAAG 2100
QY 2064 CGCAATCAATCAGTGGGCGCCACCAATGGCGCACCACTGTCTGGACACCAATCACAAG 2123
Db 2101 CTCGATCATCGGACTACGAAATGGCGTGGAGTGCAGGACGAGAGTGGCAAGATTAAA 2160
QY 2124 CTCGATCATCGGACTACGAAATGGCGTGGAGTGCAGGACGAGAGTGGCAAGATTAAA 2183
Db 2161 CATCATGACATCTCTTTTATCGACCCCTCCAGACACAAACGCTGTTGATATGAAGAT 2220
QY 2184 CATCATGACATCTCTTTTATCGACCCCTCCAGACACAAACGCTGTTGATATGAAGAT 2243
Db 2221 GTGATGGTCTCTGAATGACATCATCGAAGCGCGCTGTCTGGCACAGTCGGGCAACGAT 2280
QY 2244 GTGATGGTCTCTGAATGACATCATCGAAGCGCGCTGTCTGGCACAGTCGGGCAACGAT 2303
Db 2281 CGCGGTG-----AGGACGATGACGAGGATGGGCGGACGTTTC 2316
QY 2304 CGCGGTGCTCCGTTTACTATTTCCCAACAGAGAGCAGATGACGAGGATGGGCGGACGTTTC 2363
Db 2317 AAAGACAGGACCTCGAAGTGTCTCAAGGCATCGATGTTTGTGTGGGACTGT 2376
QY 2364 AAAGACAGGACCTCGAAGTGTCTCAAGGCATCGATGTTTGTGTGGGACTGT 2423
Db 2377 TGCTGGGTTTGGTTGAAATTTTTCAGGAGTGGGTATCGCTCATCTCTCGATCCCTTCGTC 2436
QY 2424 TGCTGGGTTTGGTTGAAATTTTTCAGGAGTGGGTATCGCTCATCTCTCGATCCCTTCGTC 2483
Db 2437 GAGCTCTTCATCAGCTGTGCATTTGTGTCAACACGATGTTTCATGGCAATGGATCACCAC 2496
QY 2484 GAGCTCTTCATCAGCTGTGCATTTGTGTCAACACGATGTTTCATGGCAATGGATCACCAC 2543
Db 2497 GATATGAACAGGAGATGGAACCGCTGCTCAAGAGTGGCAACTATTTCTTCAACCCGAC 2556
QY 2544 GATATGAACAGGAGATGGAACCGCTGCTCAAGAGTGGCAACTATTTCTTCAACCCGAC 2603

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Db	2557	TTTTGCCATCAGAGCCACCAATGAGCCTGAGCCCAAGTACTATTTCAGGAG	2616		QY	3684	AAGGCGAGCCGAGACGATGAGGCGGAGGAGAAAGCGACGCGCAAGGAGGATTTA	3743	
QY	2604	TTTTGCCATCAGAGCCACCAATGAGCCTGAGCCCAAGTACTATTTCAGGAG	2663		Db	3583	GGTCTCGAGAGAACTGACGAGGAGGCGGAATCGAGGAGGCGCCCTCGAGGGTGAT	3642	
Db	2617	GGCTGGAACTCTTCGACTTCATTATGCTGGCCCTATCGCTATTGGAATCGGACTCGAG	2676		QY	3744	GGTCTCGAGAGAACTGACGAGGAGGCGGAATCGAGGAGGCGCCCTCGAGGGTGAT	3803	
QY	2664	GGCTGGAACTCTTCGACTTCATTATGCTGGCCCTATCGCTATTGGAATCGGACTCGAG	2723		Db	3643	ATCATTTATTCATGCACACGAGGAGATATCTCGATGAATATCCAGCTGATTCGCGCCC	3702	
Db	2677	GGTGTCCAGGCTCTGCTCGGATTCGCTTTTCGATTCGCTGGCTGATTCGCTGGCC	2736		QY	3804	ATCATTTATTCATGCACACGAGGAGATATCTCGATGAATATCCAGCTGATTCGCGCCC	3863	
QY	2724	GGTGTCCAGGCTCTGCTCGGATTCGCTTTTCGATTCGCTGGCTGATTCGCTGGCC	2783		Db	3703	GATTTCGCTACTATGAAATTTCCGATCTTAGCCGGTGAAGATGATCTCGCGTTCGGCAA	3923	
Db	2737	AGTCTTGGCCACACATTAATTTACTCATTTTCGATTTATGGAGCGCACCAATGGCGCTTG	2796		QY	3864	GATTTCGCTACTATGAAATTTCCGATCTTAGCCGGTGAAGATGATCTCGCGTTCGGCAA	3923	
QY	2784	AGTCTTGGCCACACATTAATTTACTCATTTTCGATTTATGGAGCGCACCAATGGCGCTTG	2843		Db	3763	GGATGGGCAATTTACGACTGAAATCTTTTCGATTTAATTTAGAGATAAATTTTGAACA	3822	
Db	2797	GGTAATCTGACATTTGTACTTTTGCAATATCAATCTTCATCTTTGGGCGATGGGAATGCAA	2856		QY	3924	GGATGGGCAATTTACGACTGAAATCTTTTCGATTTAATTTAGAGATAAATTTTGAACA	3983	
QY	2844	GGTAATCTGACATTTGTACTTTTGCAATATCAATCTTCATCTTTGGGCGATGGGAATGCAA	2903		Db	3823	GCTGTATCTACTATGATTTAATGAGTAGCTTAGCTTTGGCATTTAGAGATGATCTG	3882	
Db	2857	CTGTTCGGAAGAAATATCATGATCACAAGACCGCTTTCCGGATGGCGACCTGCCGCG	2916		QY	3984	GCTGTATCTACTATGATTTAATGAGTAGCTTAGCTTTGGCATTTAGAGATGATCTG	4043	
QY	2904	CTGTTCGGAAGAAATATCATGATCACAAGACCGCTTTCCGGATGGCGACCTGCCGCG	2963		Db	3883	CCACAAGACCCATCTCGAGGATATTTTACTATATATGACAGAAATTTTACGGTTATA	3942	
Db	2917	TGGAACCTTCACCGACTTTATGCACAGCTTCATGATCGTTCGCGGTCTCGCGAGAA	2976		QY	4044	CCACAAGACCCATCTCGAGGATATTTTACTATATATGACAGAAATTTTACGGTTATA	4103	
QY	2964	TGGAACCTTCACCGACTTTATGCACAGCTTCATGATCGTTCGCGGTCTCGCGAGAA	3023		Db	3943	TTCTCTTTGGAAATGTTAATCAAGTGGTTCGCGCTTCAAGTGTCAAGTGTACTTGACCAAC	4002	
Db	2977	TGATCGAGTCCATGTCGACATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	3036		QY	4104	TTCTCTTTGGAAATGTTAATCAAGTGGTTCGCGCTTCAAGTGTCAAGTGTACTTGACCAAC	4163	
QY	3024	TGATCGAGTCCATGTCGACATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	3083		Db	4003	GGTGTGTGTGCTCGATTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	4062	
Db	3037	TTGGCCACCGCTTCATCGGCAATCTTTGGTACTTAACCTTTTCTAGGCTTGTCTTTG	3096		QY	4164	GGTGTGTGTGCTCGATTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	4223	
QY	3084	TTGGCCACCGCTTCATCGGCAATCTTTGGTACTTAACCTTTTCTAGGCTTGTCTTTG	3143		Db	4063	CTTGTGGAGCTGGTGGTATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG	4122	
Db	3097	TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTTCAAGTAAAGTAAAGTAAAGTAA	3156		QY	4224	CTTGTGGAGCTGGTGGTATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG	4283	
QY	3144	TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTTCAAGTAAAGTAAAGTAAAGTAA	3203		Db	4123	CCACTAGCTGCCATGTCGCGTATGAGGCGATGAGGCTGCTGCTTAAATGCGCTGGTACAA	4182	
Db	3157	GCCGAGGCTTCATCGAATTTGCGGATTTAAAGTTGGTAAAGTAAAGTAAAGTAAAGTAA	3216		QY	4284	CCACTAGCTGCCATGTCGCGTATGAGGCGATGAGGCTGCTGCTTAAATGCGCTGGTACAA	4343	
QY	3204	GCCGAGGCTTCATCGAATTTGCGGATTTAAAGTTGGTAAAGTAAAGTAAAGTAAAGTAA	3263		Db	4183	GCTATACCGCTCCATCTTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	4242	
Db	3217	TGTTTCAAGTTAATACGTAACAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAAT	3271		QY	4344	GCTATACCGCTCCATCTTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	4403	
QY	3264	TGTTTCAAGTTAATACGTAACAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAAT	3323		Db	4243	ATAATGGGTGACAGCTTTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	4302	
Db	3272	-----AGCATGGTGACACGAACTGGAGCTG	3297		QY	4404	ATAATGGGTGACAGCTTTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	4463	
QY	3324	AGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGCATGCTGACACGAACTGGAGCTG	3383		Db	4303	AAGCTCAGCCACGAGATCATACCAATTCGCAATTCGCTCGGAGAGCGAGACTACAGCTGG	4362	
Db	3298	GGCCACGAGAGATCCTCGCGAGGCTCATCAAGAGGCGGATCAAGAGGAGAGAGAGAGAA	3357		QY	4464	AAGCTCAGCCACGAGATCATACCAATTCGCAATTCGCTCGGAGAGCGAGACTACAGCTGG	4523	
QY	3384	GGCCACGAGAGATCCTCGCGAGGCTCATCAAGAGGCGGATCAAGAGGAGAGAGAGAA	3443		Db	4363	GTGAATTCAGCAATTAATTCGATCATGATAGTAAACCGCTATCTGTGCTTTTCCAAAGTG	4422	
Db	3358	CTGGAGTGGCATCGGGGATGGCAATTCAGATATACGCGGACATGAAGAACAC	3417		QY	4524	GTGAATTCAGCAATTAATTCGATCATGATAGTAAACCGCTATCTGTGCTTTTCCAAAGTG	4583	
QY	3444	CTGGAGTGGCATCGGGGATGGCAATTCAGATATACGCGGACATGAAGAACAC	3503		Db	4423	GCCACCTTCAAGAGCTGGATCAAAATCATGATCAATCATGATTCGATTCACGAGGTTGAC	4482	
Db	3418	AAGCCGAGAAATCCAAATATCTAATACGCAACG	3453		QY	4584	GCCACCTTCAAGAGCTGGATCAAAATCATGATCAATCATGATTCGATTCACGAGGTTGAC	4643	
QY	3504	AAGCCGAGAAATCCAAATATCTAATACGCAACGATGATTTGGCACTCAATTAACCAAC	3563		Db	4483	AGCAACCAATTCGTAACCAACGATCATGATGATTTATTTATTTTCGATTTCTTCATCAT	4542	
Db	3454	-----GAGCAGCAG	3462		QY	4644	AGCAACCAATTCGTAACCAACGATCATGATGATTTATTTATTTTCGATTTCTTCATCAT	4703	
QY	3564	CAAGACAATAGCTGGAACACGAGCTTAAACCATATAGAGGTTTGTCTTACAGGACGACAC	3623		Db	4543	TTTGGATCAATTTTTCACACTCAATCTGTTCAATGTTGTTTATTCATTTAATTTAATGAG	4602	
Db	3463	ACTGCCAGATTAATCTCATATGTCGCAATTAAGATTCGACCAATTAAGAGGAGAGAGCAAC	3522		QY	4704	TTTGGATCAATTTTTCACACTCAATCTGTTCAATGTTGTTTATTCATTTAATTTAATGAG	4763	
QY	3624	ACTGCCAGATTAATCTCATATGTCGCAATTAAGATTCGACCAATTAAGAGGAGAGCAAC	3683		Db	4603	CAAAAGAAAAGCAGGCTGATCATTTAGAAATGTTTCATGACAGAAAGATCAGAAAAGTAC	4662	
Db	3523	AAGGCGAGCCGAGAGAGATGGAGGCGGAGGAGAAAGCGGACCGCAGGAGGATTTA	3582						

QY 4764 CAAAGAAAAACAGGAGGATCATTAAGAAATGTTTCATGACAGAAAGATCAGAAAAAGTAC 4823
DB 4663 TATAGTGTATCAAAAGATGGCTCTAAAGAACCATTAAGCCATTCACAGACCAAGG 4722
QY 4824 TATAATGCTATGAAAAGATGGCTCTAAAGAACCATTAAGCCATTCACAGACCAAGG 4883
DB 4723 TGGCGACCAACAGCAATAGTCTTTGAAATAGTAACCGATAGAAATTCGATATATCATTT 4782
QY 4884 TGGCGACCAACAGCAATAGTCTTTGAAATAGTAACCGATAGAAATTCGATATATCATTT 4943
DB 4793 ATGTATTATTCATTGGTCTGAACATGTTACCATGACCCCTCGATCGTTAGATCGCTCGAC 4842
QY 4944 ATGTATTATTCATTGGTCTGAACATGTTACCATGACCCCTCGATCGTTAGATCGCTCGAC 5003
DB 4843 AGGTATAACGGGTCTTACAGATCTCAATGCGATATTCGTAAGTATTTTTCAGTTCGAA 4902
QY 5004 AGGTATAACGGGTCTTACAGATCTCAATGCGATATTCGTAAGTATTTTTCAGTTCGAA 5063
DB 4903 TGCTATTAAAAATATTCGCTTTACGATATCACTATTTTATTTAGCCATGGAATTTATTT 4962
QY 5064 TGCTATTAAAAATATTCGCTTTACGATATCACTATTTTATTTAGCCATGGAATTTATTT 5123
DB 4963 GATGTAGTGTGCTATTTATTCATCTTAGTCTTTGATCTTTAGGATATTTATTCAGAGAG 5022
QY 5124 GATGTAGTGTGCTATTTATTCATCTTAGTCTTTGATCTTTAGGATATTTATTCAGAGAG 5183
DB 5023 TACTTCGTCTCCGACCCCTGCTCCGAGTGTGCGTGTGGCGAAAGTGGCGCTGCTCTT 5082
QY 5184 TACTTCGTCTCCGACCCCTGCTCCGAGTGTGCGTGTGGCGAAAGTGGCGCTGCTCTT 5243
DB 5083 CGACTGGTGAAGGGAGCCAAAGGCAATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTG 5142
QY 5244 CGACTGGTGAAGGGAGCCAAAGGCAATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTG 5303
DB 5143 CCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5202
QY 5304 CCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5363
DB 5203 GGCATGTCGTTCTTCATGACGCTGAAGGAGAGAGCGGCAATTAACGACGCTCFACAACTTC 5262
QY 5364 GGCATGTCGTTCTTCATGACGCTGAAGGAGAGAGCGGCAATTAACGACGCTCFACAACTTC 5423
DB 5263 AAGACCTTTGGCCAGACGATGATCTGCTCTTTTCAGATGTCGACGTCAGCCGGTTGGAT 5322
QY 5424 AAGACCTTTGGCCAGACGATGATCTGCTCTTTTCAGATGTCGACGTCAGCCGGTTGGAT 5483
DB 5323 GGTGTACTGGAGCCCATATCAATGAGGAGCATGGATCCACCGACGACGACAAAGGC 5382
QY 5484 GGTGTACTGGAGCCCATATCAATGAGGAGCATGGATCCACCGACGACGACAAAGGC 5543
DB 5383 TATCCGGCAATTTGGTTTCAGCGACCGTTGGAATAAGCTTTCTCTCTCATACCTAGTT 5442
QY 5544 TATCCGGCAATTTGGTTTCAGCGACCGTTGGAATAAGCTTTCTCTCTCATACCTAGTT 5603
DB 5443 ATAAGCTTTTGGATAGTTATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5502
QY 5604 ATAAGCTTTTGGATAGTTATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5663
DB 5503 GCCACCGAGGAGTGAAGAGGCTTACCGACGAGGACTACGACATGTACTATGATC 5562
QY 5664 GCCACCGAGGAGTGAAGAGGCTTACCGACGAGGACTACGACATGTACTATGATC 5723
DB 5563 TGGCAGCAATTCGATCCGAGGAGCCACAGTAGTACATACGCTATGATGCTGTCGGAATTC 5622
QY 5724 TGGCAGCAATTCGATCCGAGGAGCCACAGTAGTACATACGCTATGATGCTGTCGGAATTC 5783
DB 5623 CTGGAGGTACTGGAGCCCGCTGCGAGATCCAAACCGCAAGTACAAAGTACATATG 5682
QY 5784 CTGGAGGTACTGGAGCCCGCTGCGAGATCCAAACCGCAAGTACAAAGTACATATG 5843
DB 5683 ATGGACATACCCATCTGTGCGGCTGACCTCATGTACTGGCTGACATCTCTCAGCCCTT 5742
QY 5844 ATGGACATACCCATCTGTGCGGCTGACCTCATGTACTGGCTGACATCTCTCAGCCCTT 5903

DB 5743 ACRAAGACTTCTTTGCGGGAAGGGCAATCCGATAGAGGAGAGGGGTGAGATTGGTGAG 5802
QY 5904 ACRAAGACTTCTTTGCGGGAAGGGCAATCCGATAGAGGAGAGGGGTGAGATTGGTGAG 5963
DB 5803 ATAGCGCCCGCCCGGATACGAGGGGTACGAGCCCGTCTCATCAACGCTGTGGGTGAG 5862
QY 5964 ATAGCGCCCGCCCGGATACGAGGGGTACGAGCCCGTCTCATCAACGCTGTGGGTGAG 6023
DB 5863 CGTAGGAGTACTGCGCCCGGCTAATCCAGCAGCCCTGGCGAAGACCAAGGCGCGCGGC 5922
QY 6024 CGTAGGAGTACTGCGCCCGGCTAATCCAGCAGCCCTGGCGAAGACCAAGGCGCGCGGC 6083
DB 5923 GAGGAGGTGGTCTCTTTGAGCCGGATACGATGCGGATGCGGCTGATCCCGATGCC 5982
QY 6084 GAGGAGGTGGTCTCTTTGAGCCGGATACGATGCGGATGCGGCTGATCCCGATGCC 6143
DB 5983 GGGGACCGCGCCCGGATGAAGCAACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6042
QY 6144 GGGGACCGCGCCCGGATGAAGCAACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6203
DB 6043 GTTAACGCTACTGCAAGAGGAGTCCCGATGCGGATGAGAGTAAATAGTCCGGGT 6102
QY 6204 GTTAACGCTACTGCAAGAGGAGTCCCGATGCGGATGAGAGTAAATAGTCCGGGT 6263
DB 6103 GAGGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6162
QY 6264 GAGGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6323
DB 6163 GCGGGAAGTCCCGGAGCGGCTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6222
QY 6324 GCGGGAAGTCCCGGAGCGGCTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6383
DB 6223 GGGTTCGTGACGAGAACGCGCAAGGTGTCATCCACTCGGATCCGCGGCGGCGGCGGCGGCGG 6282
QY 6384 GGGTTCGTGACGAGAACGCGCAAGGTGTCATCCACTCGGATCCGCGGCGGCGGCGGCGGCGG 6443
DB 6283 TCGCCACGCGGGGATGCTGAGCCAGGCGCTCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6342
QY 6444 TCGCCACGCGGGGATGCTGAGCCAGGCGCTCGCCCGCGGCGGCGGCGGCGGCGGCGGCGG 6503
DB 6343 TAGC 6346
QY 6504 TAGC 6507

RESULT 4
ID US-07-998-289-7 STANDARD; DNA; UNC; 5461 BP.
AC xxxxxx
DT 01-JAN-1900

DE Sequence 7, Application US/07998289.
CC Sequence 7, Application US/07998289.
CC GENERAL INFORMATION:

CC APPLICANT: Black, Bruce C.
CC APPLICANT: Taylor, Martin
CC APPLICANT: Heckel, David G.
CC TITLE OF INVENTION: Method for Monitoring Pesticide
CC TITLE OF INVENTION: Resistance
CC NUMBER OF SEQUENCES: 10

CC CORRESPONDENCE ADDRESS:
CC ADDRESS: American Cyanamid Company
CC STREET: One Cyanamid Plaza
CC CITY: Wayne
CC STATE: New Jersey
CC COUNTRY: U.S.A.
CC ZIP: 07470

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/998,289

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CC	FILING DATE: 30-DEC-1992	781	GTGCGCGCGTCATCGAATCGGTGAAGAACTCGCGGATGTGATTATCTTACCATGTTT	840
CC	CLASSIFICATION: 435	804	GTGCGCGCGTCATCGAATCGGTGAAGAACTCGCGGATGTGATTATCTTACCATGTTT	863
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Harrington, James J.			
CC	REGISTRATION NUMBER: P-38,711			
CC	REFERENCE/DOCKET NUMBER: 31,732			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: 201-831-3246			
CC	TELEFAX: 201-831-3305			
CC	INFORMATION FOR SEQ ID NO: 7:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 5461 base pairs			
CC	TYPE: nucleic acid			
CC	STRANDEDNESS: single			
CC	TOPOLOGY: linear			
CC	MOLSCULE TYPE: DNA (genomic)			
CC	Sequence 5461 BP; 1425 A; 1259 C; 1374 G; 1403 T; 0 other;			
CC	Query Match			
CC	Best Local Similarity 96.7%; Pred. No. 0.00e+00;			
CC	Matches 5445; Conservative 0; Mismatches 9; Indels 177; Gaps 3;			
Db	1 ATCACAGAGATTCGCGACTCGATATCTGAGGAAGAACGAGTTTGTTCGCTCCCTTTACC	60		
Qy	24 ATGACAGAGATTCGCGACTCGATATCTGAGGAAGAACGAGTTTGTTCGCTCCCTTTACC	83		
Db	61 CGCGAATCATTTGGTGCAATCGAACACGCTTCCGCTGAAACATGAAAGCAAGAGGAG	120		
Qy	84 CGCGAATCATTTGGTGCAATCGAACACGCTTCCGCTGAAACATGAAAGCAAGAGGAG	143		
Db	121 CTGGAAGAGAGAGCGGAGGAGAGTTCGCGGATATGTTGTCGCAAGAAACAAAAA	180		
Qy	144 CTGGAAGAGAGAGCGGAGGAGAGTTCGCGGATATGTTGTCGCAAGAAACAAAAA	203		
Db	181 GAAATCCGATATGATGACGAGGAGGATGAGGTCCCAACACCGGATCCTACACTTGA	240		
Qy	204 GAAATCCGATATGATGACGAGGAGGATGAGGTCCCAACACCGGATCCTACACTTGA	263		
Db	241 CAGGGTGCCAAATCTGTTTCGATTCGAGGAGGAGTTCGCGGAGGATTCGCGGAGG	300		
Qy	264 CAGGGTGCCAAATCTGTTTCGATTCGAGGAGGAGTTCGCGGAGGATTCGCGGAGG	323		
Db	301 COTCTCGAGGATATCGATTCCTACTACAGCAATGCTAGTACATTCGTAGTTGTAAGCAA	360		
Qy	324 COTCTCGAGGATATCGATTCCTACTACAGCAATGCTAGTACATTCGTAGTTGTAAGCAA	383		
Db	361 GGAAGAGATATTTTCGCTTTCTGCAATCAAAAGCAATGTTGATGCTGATTCATCAAT	420		
Qy	384 GGAAGAGATATTTTCGCTTTCTGCAATCAAAAGCAATGTTGATGCTGATTCATCAAT	443		
Db	421 CGGATACGTCGTGGCCATTTACATTTCTAGTGCATCCATTTATTTTCCCTATTATCATC	480		
Qy	444 CGGATACGTCGTGGCCATTTACATTTCTAGTGCATCCATTTATTTTCCCTATTATCATC	503		
Db	481 ACCACATCTCTCAACTGCATCTCTGATGATTAATGCCGCAACGCCCGGTTGAGTCC	540		
Qy	504 ACCACATCTCTCAACTGCATCTCTGATGATTAATGCCGCAACGCCCGGTTGAGTCC	563		
Db	541 ACTGAGTGATATTCACCGGATCTACATTTGATCAGCTGTTAAAGTGTAGTGCACGA	600		
Qy	564 ACTGAGTGATATTCACCGGATCTACATTTGATCAGCTGTTAAAGTGTAGTGCACGA	623		
Db	601 GGTTCATTTTATGCCGTTTACGTATCTTAGAGATGCAATGGAATGGTGGATTCGTA	660		
Qy	624 GGTTCATTTTATGCCGTTTACGTATCTTAGAGATGCAATGGAATGGTGGATTCGTA	683		
Db	661 GTAATAGCTTTAGCTTATGTCACCATGAGTATAGATTTAGGTAATCTAGCAGCTTGGGA	720		
Qy	684 GTAATAGCTTTAGCTTATGTCACCATGAGTATAGATTTAGGTAATCTAGCAGCTTGGGA	743		
Db	721 ACGTTTAGGTTGCTGCGAGGCTTAAACCGTAGCCATTTGCGCAGCTTGAAGACCATC	780		
Qy	744 ACGTTTAGGTTGCTGCGAGGCTTAAACCGTAGCCATTTGCGCAGCTTGAAGACCATC	803		

Db 1798 GAAGAGAAATGGGGCCATCATAGTGGCCGTGTACTATGCAATCTAGGCTCCGACACTCA 1857
Qy 1884 GAAGAGAAATGGGGCCATCATAGTGGCCGTGTACTATGCAATCTAGGCTCCGACACTCA 1943
Db 1858 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGGCGC 1917
Qy 1944 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGGCGC 2003
Db 1918 ATGGCCGTCATGGGGCTCAGACACATGACCAAGGAGAGCAATTCGCAACCGCAACACA 1977
Qy 2004 ATGGCCGTCATGGGGCTCAGACACATGACCAAGGAGAGCAATTCGCAACCGCAACACA 2063
Db 1978 CGCAATCAATCAGTGGGGCCACCAATGGCGCACCACTGTCTGTGACACCAATCACAAAG 2037
Qy 2064 CGCAATCAATCAGTGGGGCCACCAATGGCGCACCACTGTCTGTGACACCAATCACAAAG 2123
Db 2038 CTCGATCATCGGGACTAGCAATTTGGCTGTGAGTGCAGGAGCAAGCTGGCAAGATTTAAA 2097
Qy 2124 CTCGATCATCGGGACTAGCAATTTGGCTGTGAGTGCAGGAGCAAGCTGGCAAGATTTAAA 2183
Db 2098 CATCATGACAATCCCTTTTATCGAGCCGTCCAGACACAAAGCGTGTGTATGAAAGAT 2157
Qy 2184 CATCATGACAATCCCTTTTATCGAGCCGTCCAGACACAAAGCGTGTGTATGAAAGAT 2243
Db 2158 GTGATGGTCTGAAATGACATCATCAAGACAGCGCGTGTGCGACAGTCGGGCAACGAT 2217
Qy 2244 GTGATGGTCTGAAATGACATCATCAAGACAGCGCGTGTGCGACAGTCGGGCAACGAT 2303
Db 2218 CGCGTGTCTCGGTTTACTATTTCCTCAACAGAGACAGATGACGAGGATGGCGGACGTTT 2277
Qy 2304 CGCGTGTCTCGGTTTACTATTTCCTCAACAGAGACAGATGACGAGGATGGCGGACGTTT 2363
Db 2278 AAAGACAAGGCACTCGAAGTGTATCTCAAGGCACTCGATGTGTTTGTGTGGGACGT 2337
Qy 2364 AAAGACAAGGCACTCGAAGTGTATCTCAAGGCACTCGATGTGTTTGTGTGGGACGT 2423
Db 2338 TGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTCGTC 2397
Qy 2424 TGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTCGTC 2483
Db 2398 GAGCTCTTCATCAGCTGTGCATTTGTGTCAACAGATGTTTCATGGCAATGGATCACCAC 2457
Qy 2484 GAGCTCTTCATCAGCTGTGCATTTGTGTCAACAGATGTTTCATGGCAATGGATCACCAC 2543
Db 2458 GATATGAACAAGGAGATGAAGCGTGTCTCAAGAGTGGCAACTATTTCTTCAACGCCACC 2517
Qy 2544 GATATGAACAAGGAGATGAAGCGTGTCTCAAGAGTGGCAACTATTTCTTCAACGCCACC 2603
Db 2518 TTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCCAAGTACTATTTCCAGGAG 2577
Qy 2604 TTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCCAAGTACTATTTCCAGGAG 2663
Db 2578 GCGTGGACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTTGGAATGGGACTCGAG 2637
Qy 2664 GCGTGGACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTTGGAATGGGACTCGAG 2723
Db 2638 GGTGTCCAGGGTCTGTCGATTTGGTTCCTTTTCGATTCGCTGCTGTTTCAAACTGGCC 2697
Qy 2724 GGTGTCCAGGGTCTGTCGATTTGGTTCCTTTTCGATTCGCTGCTGTTTCAAACTGGCC 2783
Db 2698 AAGTCTTGGCCCCACACTTAATTTACTCATTTTCGATTTATGGGACGACCATTGGGCGCTTTG 2757
Qy 2784 AAGTCTTGGCCCCACACTTAATTTACTCATTTTCGATTTATGGGACGACCATTGGGCGCTTTG 2843
Db 2758 GGTATCTGACATTTGTACTTTGCAATTTATCATCTTCATCTTTGGCGGTGATGGGAATGCAA 2817
Qy 2844 GGTATCTGACATTTGTACTTTGCAATTTATCATCTTCATCTTTGGCGGTGATGGGAATGCAA 2903
Db 2818 CTGTTCCGGAAGAATATCATGATCAGAGGACCGCTTTCCGGATGGCGACCTGCCGGC 2877
Qy 2904 CTGTTCCGGAAGAATATCATGATCAGAGGACCGCTTTCCGGATGGCGACCTGCCGGC 2963
Db 2878 TGGAACTTCACCGACTTTTATGACACAGCTTCATGATCGTGTTCGGGTGTCTCTGCGGAGAA 2937

Qy 2964 TGGAACTTCACCGACTTTTATGACACAGCTTCATGATCGTGTTCGGGTGTCTCTGCGGAGAA 3023
Db 2938 TGGATCAGATCCATGTGGGACTGCATGTACGTGGCGGATGTCTCGTGCATTTCCCTTCTTC 2997
Qy 3024 TGGATCAGATCCATGTGGGACTGCATGTACGTGGCGGATGTCTCGTGCATTTCCCTTCTTC 3083
Db 2998 TTTGCCACCGTGTGTATCGGCAATCTTGTGTACTTTAACTTTTCTAGCCTTCTGCTTTTG 3057
Qy 3084 TTTGCCACCGTGTGTATCGGCAATCTTGTGTACTTTAACTTTTCTAGCCTTCTGCTTTTG 3143
Db 3058 TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAAATA 3117
Qy 3144 TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAAATA 3203
Db 3118 GCCGAGGCTTCAATCGAATTTGGCGGATTTAAAGTTTGGGTTTAAAGCTTAATTTGCTGAT 3177
Qy 3204 GCCGAGGCTTCAATCGAATTTGGCGGATTTAAAGTTTGGGTTTAAAGCTTAATTTGCTGAT 3263
Db 3178 TGTTCAGTTTAACTACGTAAACAAATTTGACAAATCAAAATAGTGTCAACCATCAG----- 3232
Qy 3264 TGTTCAGTTTAACTACGTAAACAAATTTGACAAATCAAAATAGTGTCAACCATCAGTTGAG 3323
Db 3233 -----AGCATGTGTGACAAACGAACTGGAGCTG 3258
Qy 3324 AGGACCAACCAAGATCAGTTGGATTTGGAGCGAAGAGCATGTGTGACAAACGAACTGGAGCTG 3383
Db 3259 GGCCACGACGAGATCTCTCGCGAGCGGCTCATCAAGAGGGGATCAAGGACGACAGCGAA 3318
Qy 3384 GGCCACGACGAGATCTCTCGCGAGCGGCTCATCAAGAGGGGATCAAGGACGACAGCGAA 3443
Db 3319 CTGAGGTGGGCACTCGGGGATGGATTTACGATACACGCGGACATCAAGAAACAAAC 3378
Qy 3444 CTGAGGTGGGCACTCGGGGATCGGATGGATTTACGATACACGCGGACATCAAGAAACAAAC 3503
Db 3379 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACG----- 3414
Qy 3504 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATTTGGCAACTCAATTAACCCAC 3563
Db 3415 -----GACGACGAC 3423
Qy 3564 CAAGACAATGACTGGAAACAGACGCTAAACATAGAGTTTGTCTTACAGGACGACGAC 3623
Db 3424 ACTGCCAGCTTAATCTATGTTAGCCATTAAGAAATCAACCATTAAGAGGACGAGAGCCAC 3483
Qy 3624 ACTGCCAGCTTAATCTATGTTAGCCATTAAGAAATCAACCATTAAGAGGACGAGAGCCAC 3683
Db 3484 AAGGCAAGCCGCGAGACGATGGAGGGGAGAGAAAGCGGACGCGACGCAAGGAGGATTTA 3543
Qy 3684 AAGGCAAGCCGCGAGACGATGGAGGGGAGAGAAAGCGGACGCGACGCAAGGAGGATTTA 3743
Db 3544 GGTCTCGAGGAGGAACTGGAGGAGGGGCAATTCGAGGAGGGCCGCTCGACGGTGTAT 3603
Qy 3744 GGTCTCGAGGAGGAACTGGAGGAGGGGCAATTCGAGGAGGGCCGCTCGACGGTGTAT 3803
Db 3604 ATCATTTATTCACACGACGAGGATATACTCGATGAATATCCAGCTGATTGTGTCGCC 3663
Qy 3804 ATCATTTATTCACACGACGAGGATATACTCGATGAATATCCAGCTGATTGTGTCGCC 3863
Db 3664 GATTCTGATATAAGAAATTTCCGATCTTAGCCGCTGACGATGACTCCGCCGTTCTGGCAA 3723
Qy 3864 GATTCTGATATAAGAAATTTCCGATCTTAGCCGCTGACGATGACTCCGCCGTTCTGGCAA 3923
Db 3724 GGATGGGCAATTTACGACTGAAAACCTTTTCGATTAATTTAGGATAAATAATTTTGAACA 3783
Qy 3924 GGATGGGCAATTTACGACTGAAAACCTTTTCGATTAATTTAGGATAAATAATTTTGAACA 3983
Db 3784 GCTGTATCTACTATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG 3843
Qy 3984 GCTGTATCTACTATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG 4043
Db 3844 CCACAAAGACCCACTACTCGAGGATATTTTACTATATGACAGAAATTTTACGGTTATA 3903

4044	CCACAAGACCCACTCTCCAGGATATTTATACTATATGACAGAAATATTTACGGTTATA	4103
3904	TTCTTCTTTGGAAATGTTAAATCAAGTGGTTGGCGTCGGCTTCAAGGTACTTTGACCAAC	3963
4104	TTCTTCTTTGGAAATGTTAAATCAAGTGGTTGGCGTCGGCTTCAAGGTACTTTACCAAC	4163
3964	GGTGGTGTGGCTCGATTTGGTGATGTCATGTGATCGCTTATCAACTTCGTTGCTTCA	4023
4164	GGTGGTGTGGCTCGATTTGGTGATGTCATGTGATCGCTTATCAACTTCGTTGCTTCA	4223
4024	CTTGTGGAGCTGGTGGTATTCAGACCTTCAAGACTATGCCAAGCTTTAAGAGCACTGAGA	4083
4224	CTTGTGGAGCTGGTGGTATTCAGACCTTCAAGACTATGCCAAGCTTTAAGAGCACTGAGA	4283
4084	CCACTACGTGCCATGTCGCCGTATGCAGGCGATGAGGGTCGCTGTTAATGCGCTGGTCAA	4143
4284	CCACTACGTGCCATGTCGCCGTATGCAGGCGATGAGGGTCGCTGTTAATGCGCTGGTCAA	4343
4144	GCTATACCGTCCACTTCTCAATGCTGTTGGTGTGTCATAATTTTGGCTAATTTTGGCT	4203
4344	GCTATACCGTCCACTTCTCAATGCTGTTGGTGTGTCATAATTTTGGCTAATTTTGGCT	4403
4204	ATAATGGGTGTACAGCTTTTGGCTGAAAATAATTTTAAAGTGGGAGACATGAATGGCAGG	4263
4404	ATAATGGGTGTACAGCTTTTGGCTGAAAATAATTTTAAAGTGGGAGACATGAATGGCAGG	4463
4264	AAGCTCAGCCACGAGATCATACCAATTCGCAATGCCATGGGAGCGAGCACTACAGTGG	4323
4464	AAGCTCAGCCACGAGATCATACCAATTCGCAATGCCATGGGAGCGAGCACTACAGTGG	4523
4324	GTGAATTCAGCAATGAATTTTCGATCATGTAGTAAAGCGCTATCTGTGCCTTTTCCAAGTG	4383
4524	GTGAATTCAGCAATGAATTTTCGATCATGTAGTAAAGCGCTATCTGTGCCTTTTCCAAGTG	4583
4384	GCCACCTTCAAGGCTGGATACAAATCATGAAGTCTATCGATTCAGTACAGAGAGTGGAC	4443
4584	GCCACCTTCAAGGCTGGATACAAATCATGAAGTCTATCGATTCAGTACAGAGAGTGGAC	4643
4444	AAGCAACCAATTCGTAACCAACATCTACATGTATTTATTTATTTTCGTATTTCTTCATCAT	4503
4644	AAGCAACCAATTCGTAACCAACATCTACATGTATTTATTTATTTTCGTATTTCTTCATCAT	4703
4504	TTTGGATCATTTTTCCACACTCAATCTGTTCAATGGTGTATCATTTGATATTTAATGAG	4563
4704	TTTGGATCTTTTTCCACACTCAATCTGTTCAATGGTGTATCATTTGATATTTAATGAG	4763
4564	CAAAAGAAAAAGCAGGTGGATCTAGAAATTTGTCATGACAGAGATCAGAAAAAGTAC	4623
4764	CAAAAGAAAAAGCAGGTGGATCTAGAAATTTGTCATGACAGAGATCAGAAAAAGTAC	4823
4624	TATAGTGTCTATGAAAAGATGGGCTCTAAAAACCATTAAAGCCATTCGAAGACCAAGG	4683
4824	TATATAGTGTATGAAAAGATGGGCTCTAAAAACCATTAAAGCCATTCGAAGACCAAGG	4883
4684	TGGCGACCAACGACATAGCTTTTGGAAATAGTAACCGATAAGAAAAATTCGATATATCAT	4743
4884	TGGCGACCAACGACATAGCTTTTGGAAATAGTAACCGATAAGAAAAATTCGATATATCAT	4943
4744	ATGTTATTCATTTGGTCTGTAACATGTTCCACATGACCCCTCGATTCAGTCGCTCGAC	4803
4944	ATGTTATTCATTTGGTCTGTAACATGTTCCACATGACCCCTCGATTCAGTCGCTCGAC	5003
4804	ACGTTATACGGGTCCTAGACTATCTCAATGCCATATTCGTAGTTATTTTCAGTTCGGAA	4863
5004	ACGTTATACGGGTCCTAGACTATCTCAATGCCATATTCGTAGTTATTTTCAGTTCGGAA	5063
4864	TGTCCTATTAATAATTTTCGCTTTACGATATCACTATTTTATTCAGCCATGGATTTATTT	4923
5064	TGTCCTATTAATAATTTTCGCTTTACGATATCACTATTTTATTCAGCCATGGATTTATTT	5123
4924	GATGTAGTAGTTGTTCATTTTATCCATCTTAGGCTTCTTACTTAGCGATATATTCGAGAAG	4983
5124	GATGTAGTAGTTGTTCATTTTATCCATCTTAGGCTTCTTACTTAGCGATATATTCGAGAAG	5183

4984	TACTTGTGTGCGCGACCTGCTCCGAGTGTGCGTGTGGCGAAGTGGCGCGTGTGCTTT	5043
4985		
5184	TACTTGTGTGCGCGACCTGCTCCGAGTGTGCGTGTGGCGAAGTGGCGCGTGTGCTTT	5243
5185		
5044	CGACTGTGTGAAGGAGCGCAAGGGCATTCGGACACTGCTTTCGGGTTGGCCATGTCGCTG	5103
5045		
5244	CGACTGTGTGAAGGAGCGCAAGGGCATTCGGACACTGCTTTCGGGTTGGCCATGTCGCTG	5303
5245		
5104	CGGGCCCTGTTTCAACATCTGCCTGCTGCTTTCCTCGGTTCATGTTTCGCAATTTTC	5163
5105		
5304	CGGGCCCTGTTTCAACATCTGCCTGCTGCTTTCCTCGGTTCATGTTTCGCAATTTTC	5363
5305		
5164	GGCATGTCGTTCTTCATGCGAGTGAAGGAGCGGCATTAAACGAGTCTTACAACTTC	5223
5165		
5364	GGCATGTCGTTCTTCATGCGAGTGAAGGAGCGGCATTAAACGAGTCTTACAACTTC	5423
5365		
5224	AGACCTTTGGCCAGAGCATGATCCTGCTCTTTTCAGATGTCAGCTCAGCCGGTTGGAT	5283
5225		
5424	AGACCTTTGGCCAGAGCATGATCCTGCTCTTTTCAGATGTCAGCTCAGCCGGTTGGAT	5483
5425		
5284	GGTGTACTGGAGCGCCATTATCAANTGAGGAGCATGCGATCCACCCGACGACAAAGGC	5343
5285		
5484	GGTGTACTGGAGCGCCATTATCAANTGAGGAGCATGCGATCCACCCGACGACAAAGGC	5543
5485		
5344	TATCCGGGCAATTTGGTTCAGCGACCGTTGGAATAACGTTTCTCTCTCATACCTAGTT	5403
5345		
5544	TATCCGGGCAATTTGGTTCAGCGACCGTTGGAATAACGTTTCTCTCTCATACCTAGTT	5603
5545		
5404	ATAAGCTTTTGATAGTTTATTAATGATGACATTCGTCATCTTCGAGAAC	5454
5405		
5604	ATAAGCTTTTGATAGTTTATTAATGATGACATTCGTCATCTTCGAGAAC	5654
5605		
RESULT 5		
US	-07-998-289B-7 STANDARD; DNA: UNC; 5461 BP.	
ID	AC	xxxxxx
AC	01-JAN-1900	
DT	Sequence 7, Application US/07998289B.	
DE	Sequence 7, Application US/07998289B	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Black, Bruce C	
CC	APPLICANT: Taylor, Martin	
CC	APPLICANT: Heckel, David G	
CC	TITLE OF INVENTION: Method for Monitoring Pesticide	
CC	TITLE OF INVENTION: Resistance	
CC	NUMBER OF SEQUENCES: 40	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Darby & Darby PC	
CC	STREET: 805 Third Avenue	
CC	CITY: New York	
CC	STATE: New York	
CC	COUNTRY: US	
CC	ZIP: 10022	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: Patentin Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/07/998,289B	
CC	FILING DATE: 30-DEC-1992	
CC	CLASSIFICATION: 435	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Robinson, Joseph R	
CC	REGISTRATION NUMBER: 33,448	
CC	REFERENCE/DOCKET NUMBER: 0646/0A939	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: 212-527-7700	
CC	TELEFAX: 212-753-6237	
CC	TELEX: 236687	
CC	INFORMATION FOR SEQ ID NO: 7:	
CC	SEQUENCE CHARACTERISTICS:	
CC		

CC LENGTH: 5461 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
SQ Sequence 5461 BP; 1425 A; 1259 C; 1374 G; 1403 T; 0 other;

Query Match 67.2%; Score 4374; DB 15; Length 5461;
Best Local Similarity 96.7%; Pred. No. 0.00e+00;
Matches 5445; Conservative 0; Mismatches 9; Indels 177; Gaps 3;

Db 1 ATGACAGAGATTCCGACTCGATATCTGTAGGAAGAACGAGTTTGTTCGTCCTTTACC 60
Qy 24 ATGACAGAGATTCCGACTCGATATCTGTAGGAAGAACGAGTTTGTTCGTCCTTTACC 83
Db 61 CCGCAATCATTGGTCAATCAACACGCGATGCGCTGACATGAAGAGCAGAGAG 120
Qy 84 CCGCAATCATTGGTCAATCAACACGCGATGCGCTGACATGAAGAGCAGAGAG 143
Db 121 CTGGAAAGAAAGAGAGCCGAGGAGGTGCGCGGATATGGTTCGCAAGAAAAACAAAA 180
Qy 144 CTGGAAAGAAAGAGAGCCGAGGAGGTGCGCGGATATGGTTCGCAAGAAAAACAAAA 203
Db 181 GAAATCCGATATGATGACGAGACGAGGATGAAGTTCACAAACCGGATCCTACACTTGA 240
Qy 204 GAAATCCGATATGATGACGAGACGAGGATGAAGTTCACAAACCGGATCCTACACTTGA 263
Db 241 CAGGCTGTCCCAATACCTCTTGGATGCGAGGCGAGCTTCCCGCGGAATGCGCTCCACT 300
Qy 264 CAGGCTGTCCCAATACCTCTTGGATGCGAGGCGAGCTTCCCGCGGAATGCGCTCCACT 323
Db 301 CCTCTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTCGTAGTTGTAAGCAA 360
Qy 324 CCTCTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTCGTAGTTGTAAGCAA 383
Db 361 GGAAGAAGATATTTTCGCTTTTCTGCAATCAAGCAATGTGATGCTCGATCCATCAAT 420
Qy 384 GGAAGAAGATATTTTCGCTTTTCTGCAATCAAGCAATGTGATGCTCGATCCATCAAT 443
Db 421 CGGATACGTCGTTGGCCATTACATCTTCTAGTGCATCCATTATTTCCCTATTTCATCATC 480
Qy 444 CGGATACGTCGTTGGCCATTACATCTTCTAGTGCATCCATTATTTCCCTATTTCATCATC 503
Db 481 ACCACAATTTCTCGTCAACTGTCATCTGATGATAAATGCCGACACGCCCGTTGAGTCC 540
Qy 504 ACCACAATTTCTCGTCAACTGTCATCTGATGATAAATGCCGACACGCCCGTTGAGTCC 563
Db 541 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTGGCAGCA 600
Qy 564 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTGGCAGCA 623
Db 601 GGTTCATTTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTA 660
Qy 624 GGTTCATTTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTA 683
Db 661 GTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATTTAGGTAATCTAGCAGCCCTGCCA 720
Qy 684 GTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATTTAGGTAATCTAGCAGCCCTGCCA 743
Db 721 AGTTTAGGGTGTGGCAGCGCTTAAACCGTAGCCATTTGTCGAGGCTTGAAGACCATC 780
Qy 744 AGTTTAGGGTGTGGCAGCGCTTAAACCGTAGCCATTTGTCGAGGCTTGAAGACCATC 803
Db 781 GTCGCGCGCTCATCGAATCGGTGAAGAATCTGCGGGATGTGATATCTTGACCATGTTTC 840
Qy 804 GTCGCGCGCTCATCGAATCGGTGAAGAATCTGCGGGATGTGATATCTTGACCATGTTTC 863
Db 841 TCCCTGTGCGGTGTCGCTTGTAGTGGCCTACAGATCTATATGGCGGTGCTCACCGAGAG 900
Qy 864 TCCCTGTGCGGTGTCGCTTGTAGTGGCCTACAGATCTATATGGCGGTGCTCACCGAGAG 923
Db 901 TGCATCAAGAAGTTCCCGTGTGACGGTTTCCGTGGGCAATCTTGACCGACGAGACTGGGAC 960

Qy 924 TGCATCAAGAAGTTCCCGCTGGAGGGTTCTTGGGCAATCTGACCGAGAGAACTGGAC 983
Db 961 TATCAATTCGAATAGCTCCAAATTTGGTATTCCGAGGACGAGGCGATCTCATTTCCGTTA 1020
Qy 984 TATCAATTCGAATAGCTCCAAATTTGGTATTCCGAGGACGAGGCGATCTCATTTCCGTTA 1043
Db 1021 TCGGCAATATATCCGTTGCGGGCAATTCGACGACGATACGTTGCTGCTGCAGGGGTTT 1080
Qy 1044 TCGGCAATATATCCGTTGCGGGCAATTCGACGACGATACGTTGCTGCTGCAGGGGTTT 1103
Db 1081 GGTCCGAATTCGAATATGCTGTACACAGCTTCGATTCGTTGCGGATGGGCTTTCTGTCC 1140
Qy 1104 GGTCCGAATTCGAATATGCTGTACACAGCTTCGATTCGTTGCGGATGGGCTTTCTGTCC 1163
Db 1141 GCTTCCCGCTGTACACAGAGACTTCTGGAGGATCTGTACACGCTGGTGTGGCGGCC 1200
Qy 1164 GCTTCCCGCTGTACACAGAGACTTCTGGAGGATCTGTACACGCTGGTGTGGCGGCC 1223
Db 1201 CCGGACCATGSCACATGCTGTTCTTTATAGTCATCATCTTCTAGTTTCATTTCTATCTT 1260
Qy 1224 CCGGACCATGSCACATGCTGTTCTTTATAGTCATCATCTTCTAGTTTCATTTCTATCTT 1283
Db 1261 GTGAATTTGATTTGGCCATTGTTGCCATGCTGTATGACGAATTCGAAGAGAGCCGAA 1320
Qy 1284 GTGAATTTGATTTGGCCATTGTTGCCATGCTGTATGACGAATTCGAAGAGAGCCGAA 1343
Db 1321 GAAGAAGAGGCTGCCGAAGAGAGGCGATACGTGAAGCGGAAGAGCTGCCGCCGCCAAA 1380
Qy 1344 GAAGAAGAGGCTGCCGAAGAGAGGCGATACGTGAAGCGGAAGAGCTGCCGCCGCCAAA 1403
Db 1381 GCGGCCAAGCTGGAGAGCGGSCCAATCGCAGGCTCAGGCGAGCAGCGGATGCGGCTGCC 1440
Qy 1404 GCGGCCAAGCTGGAGAGCGGSCCAATCGCAGGCTCAGGCGAGCAGCGGATGCGGCTGCC 1463
Db 1441 GCGGAAGAGGCTGCATCCGGAATGSCCAAGAGTCCGACGATATCTTGCATCAGC 1500
Qy 1464 GCGGAAGAGGCTGCATCCGGAATGSCCAAGAGTCCGACGATATCTTGCATCAGC 1523
Db 1501 TATGAGCTATTGTTGGCGGCGAGAGGCAACGATGACAAACAAAGAGAGATGTC 1560
Qy 1524 TATGAGCTATTGTTGGCGGCGAGAGGCAACGATGACAAACAAAGAGAGATGTC 1583
Db 1561 ATTCCGAGCGTGGAGTGGAGTGGAGTGGTGGAGCTTATACAAAGACAAACAGCACCT 1620
Qy 1584 ATTCCGAGCGTGGAGTGGAGTGGAGTGGTGGAGCTTATACAAAGACAAACAGCACCT 1643
Db 1621 ACCACAGCACCAAGCTACCAAAAGTTTCTGTAAGTGAGCAGC----- 1662
Qy 1644 ACCACAGCACCAAGCTACCAAAAGTTTCTGTAAGTGAGCAGCAGATCTTATCTTACCT 1703
Db 1663 -----TACACGATACGGAAC 1677
Qy 1704 GGTTCACCGTTTAACATACGCGAGGGGATCAGTAGTTCTCACAAGTACAGTACGGAAC 1763
Db 1678 GGACGTGGCGGCTTTGGTATACCCGGTAGCGATCGTAAGCCATTTGGTATTTGTAACATAT 1737
Qy 1764 GGACGTGGCGGCTTTGGTATACCCGGTAGCGATCGTAAGCCATTTGGTATTTGTAACATAT 1823
Db 1738 CAGGATGCCAGCAGCAGCTTGCCCTATGCCGACGACTCGAATGCGCTCACCCCGATGTC 1797
Qy 1824 CAGGATGCCAGCAGCAGCTTGCCCTATGCCGACGACTCGAATGCGCTCACCCCGATGTC 1883
Db 1798 GAAGAAGATGGGGCCATCATAGTGCCTGTACTATGGCAATCTAGGCTCCCGACACTCA 1857
Qy 1884 GAAGAAGATGGGGCCATCATAGTGCCTGTACTATGGCAATCTAGGCTCCCGACACTCA 1943
Db 1858 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGCGGC 1917
Qy 1944 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGCGGC 2003
Db 1918 ATGGCGCGTATGGGCGTCCAGCAATGACCAAGAGAGCAATTTGCGCAACCGCAACACA 1977
Qy 2004 ATGGCGCGTATGGGCGTCCAGCAATGACCAAGAGAGCAATTTGCGCAACCGCAACACA 2063

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Db	1978	CGCAATCAATCAGTGGGCGCCACCAATGCGGCGCACACCTGTCTGGACACCAATCACAG	2037
Qy	2064	CGCAATCAATCAGTGGGCGCCACCAATGCGGCGCACACCTGTCTGGACACCAATCACAG	2123
Db	2038	CTCGATCATCGGCTAGCAAAATGGCTGGAGTGCACGACGAAGCTGGCAAGATTAA	2097
Qy	2124	CTCGATCATCGGCTAGCAAAATGGCTGGAGTGCACGACGAAGCTGGCAAGATTAA	2183
Db	2098	CATCATGACAACTCTTTATTCGAGCCCGTCCAGACACAAACGGTGTGTATGAAAGAT	2157
Qy	2184	CATCATGACAACTCTTTATTCGAGCCCGTCCAGACACAAACGGTGTGTATGAAAGAT	2243
Db	2158	GTGATGGTCTGATGACATCATCGAACAGCCGCTGTCGCGACACAGTCCGGCAACGGAT	2217
Qy	2244	GTGATGGTCTGATGACATCATCGAACAGCCGCTGTCGCGACACAGTCCGGCAACGGAT	2303
Db	2218	CGCGGTGTCTCGGTTACTATTTCCCAACAGAGGACGATGACGAGGATGGCGGACGTTT	2277
Qy	2304	CGCGGTGTCTCGGTTACTATTTCCCAACAGAGGACGATGACGAGGATGGCGGACGTTT	2363
Db	2278	AAAGACAAGGCACTCGAAGTGTCTCAAGGCAATCGATGTTTGTGTGGGACTGT	2337
Qy	2364	AAAGACAAGGCACTCGAAGTGTCTCAAGGCAATCGATGTTTGTGTGGGACTGT	2423
Db	2338	TGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTATGCTCATCTGCTTCGATCCCTTCGTC	2397
Qy	2424	TGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTATGCTCATCTGCTTCGATCCCTTCGTC	2483
Db	2398	GAGCTCTTCATCAGCTGTGCAATTTGCTCAACAGGATGTTTCATGGCAATGGATCACAC	2457
Qy	2484	GAGCTCTTCATCAGCTGTGCAATTTGCTCAACAGGATGTTTCATGGCAATGGATCACAC	2543
Db	2458	GATATGAACAAGGAGATGGAAGCGTGTCTCAAGAGTGGCAACTATTTCTTCACCGCCACC	2517
Qy	2544	GATATGAACAAGGAGATGGAAGCGTGTCTCAAGAGTGGCAACTATTTCTTCACCGCCACC	2603
Db	2518	TTTGCCATCAGGCGCCACCATGAAGCTAATGGCCATGAGCCCAAGTACTATTTCAGGAG	2577
Qy	2604	TTTGCCATCAGGCGCCACCATGAAGCTAATGGCCATGAGCCCAAGTACTATTTCAGGAG	2663
Db	2578	GGCTGGAACATCTTCGACTTCAATTCGTCGGCCCTATCTGCTATTTGGAATGGGACTCGAG	2637
Qy	2664	GGCTGGAACATCTTCGACTTCAATTCGTCGGCCCTATCTGCTATTTGGAATGGGACTCGAG	2723
Db	2638	GGGTCCAGGCTGTCCGTTATTCGATTTCTTTTCGATTTCTGCTGTTATTCAACTGGCC	2697
Qy	2724	GGGTCCAGGCTGTCCGTTATTCGATTTCTTTTCGATTTCTGCTGTTATTCAACTGGCC	2783
Db	2698	AACTTTTGGCCACACTTAATTTACTTCATTTGATTTGAGGCGCACCATGGCGGCTTTG	2757
Qy	2784	AACTTTTGGCCACACTTAATTTACTTCATTTGATTTGAGGCGCACCATGGCGGCTTTG	2843
Db	2758	GGTAATCTGACATTTGACTTTGATTTATCTTCTTCTGCTGCTGTTATTCAACTGGCA	2817
Qy	2844	GGTAATCTGACATTTGACTTTGATTTATCTTCTTCTGCTGCTGTTATTCAACTGGCA	2903
Db	2818	CTGTTCCGGAAGAAATATCATGATCACAAGGACCGCTTTCGGATGCGGACCTGCGCGC	2877
Qy	2904	CTGTTCCGGAAGAAATATCATGATCACAAGGACCGCTTTCGGATGCGGACCTGCGCGC	2963
Db	2878	TGGAACCTTCACCGACTTATGACAGCTTCATGATCGTGTTCGCGTCTCTGGGAGAA	2937
Qy	2964	TGGAACCTTCACCGACTTATGACAGCTTCATGATCGTGTTCGCGTCTCTGGGAGAA	3023
Db	2938	TGATCGAGTCCGATGGGACTGCAATGACGTGGGCGGATGCTCGTGCATTCCTTCCTTC	2997
Qy	3024	TGATCGAGTCCGATGGGACTGCAATGACGTGGGCGGATGCTCGTGCATTCCTTCCTTC	3083
Db	2998	TTGGCCACCGCTGTCTACGCGCAATCTGTGGTACTTAACCTTTTCTTAGCCTTGCTTTG	3057
Qy	3084	TTGGCCACCGCTGTCTACGCGCAATCTGTGGTACTTAACCTTTTCTTAGCCTTGCTTTG	3143
Db	3058	TCGAATTTTGGCTCATCTAGCTTATCAGCGGCTGCTGCGGATACGATACGATAAATA	3117
Qy	3144	TCGAATTTTGGCTCATCTAGCTTATCAGCGGCTGCTGCGGATACGATACGATAAATA	3203
Db	3118	GCGGAGCCCTTCAATCGAATTTGGCCGATTTAAAGTTGGGTTAAGCGTAATTTCTGAT	3177
Qy	3204	GCGGAGCCCTTCAATCGAATTTGGCCGATTTAAAGTTGGGTTAAGCGTAATTTCTGAT	3263
Db	3178	TGTTTCAAGTTAATCGTAACTAATTTGACAAATCAAAATGAATGATCAACCATCAGGTGAG	3232
Qy	3264	TGTTTCAAGTTAATCGTAACTAATTTGACAAATCAAAATGAATGATCAACCATCAGGTGAG	3323
Db	3233	-----AGCATGGTGACAAACCAACATCAACCATCAGGTGAG	3258
Qy	3324	AGGACCAACAGATCAGTTGATTTGGAGGAGAGATGTTGACAAACATTTGAGCTG	3383
Db	3259	GGCCACGACGAGATCTTCGCGGAGGCTTCATCAAGAGGGGATCAAGGAGCAGACGCA	3318
Qy	3384	GGCCACGACGAGATCTTCGCGGAGGCTTCATCAAGAGGGGATCAAGGAGCAGACGCA	3443
Db	3319	CTGGAGTGGCCATCGGGGATGGCATGGAATTCACGATACACGCGGACATGAAGAACA	3378
Qy	3444	CTGGAGTGGCCATCGGGGATGGCATGGAATTCACGATACACGCGGACATGAAGAACA	3503
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Db 5845 GGTGAAATTTGATAGTAGCGGCGGACCGGACGAGGCTATGATCCGCTGCTGCTCA 5904
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QY 6009 AGCTGTGGCTGAGCTGAGGAGTACTGCGCCGCTAATCCAGCAGCGCTGGCG 6064

RESULT 7
ID US-08-808-793-2 STANDARD; DNA; UNC; 6315 BP.
AC XXXXX
DE 01-JAN-1900
Sequence 2, Application US/08808793.
Sequence 2, Application US/08808793
GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC TITLE OF INVENTION: AND USE THEREOF
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC STREET: Clinton Square, P.O. Box 1051
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/808,793
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/034,361
CC FILING DATE: 24-DEC-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/012,649
CC FILING DATE: 01-MAR-1996
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Braman, Susan J.
CC REGISTRATION NUMBER: 34,103

CC REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 716-263-1636

CC TELEFAX: 716-263-1600

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 6315 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

CC SINGLEDNESS: single
CC TOPOLOGY: linear

CC	TOPOLOGY: TUBUL
CC	MOLECULE TYPE: CDNA

CC	MOLECULE TYPE:	CDNA
SO	Sequence	6315 BP: 1711 A: 1344 C: 1595 G: 1665 T: 0 other:

Query Match 56.3%: Score 3664: DB 70: Length 6315:

Query Match: 50.50; Score: 5004; DB: 70;
Best Local Similarity: 84.88; Pred. No. 0.00e+00;

Best local similarity	94.0%	Freq. NO:	0.00e+00;
Matches	4980:	Conservative	0: Mismatches 812:
			Indels 84: Gaps 21:

Db 151 ATACGATATGACGAGGACGAAGATGAAGGTCCACAGCCGGATCCCACACTTGAACAG 210

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

OV 207 ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGAACAG 266

THE UNIVERSITY OF CHICAGO

D_b 211 GG GTG GCG CTA TAC CTT GTT CGA ATG CAG GCG CAG CTT CCC GCG CGG AAT TGG CCT CCA CTC CT 270

QY 267 GGTGTGCCAATACCTGTTCGATTGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT 326

Db 271 CTCGAGGATATCGATCCCTTCTACAGTAATGTACTGACATTGTAGTAATAAGTAAAGGA 330

QY 327 CTCGAGGATATCGATCCCTACTACAGCAATGTACTGTAGTTGTAAGCAAAGGA 386

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D6 331 AAGGATAATTTTCGTTTTCTGCCCTCAAAGCAATGTGGCTGCTCGATCCATTCAATCCG 390

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38 / AAAGATATATTTTCGCTTTTCGCAATCAAAGCAATGTGGATGCTCGATCCATTCAAATCCG 446

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[illegible]

Db 451 ACTATTCTAACTAATTGTATTTTAAATGATAATGCCGACAACGCCACGGTCGAATCCACA 510

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QY 507 ACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAAACGCCAGGTGAGTCCACT 566

Db 511 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT 570

QY 567 GAGTGATATTCACCGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCAGAGGT 626

D_b 571 TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTA 630

QY	3192	ACGAAATAAATAGCCGAGCGCTTCAATCGAATTTGGCGGATTTAAAAAGTTGGGTAAAGCGT	3251
DB	3184	ATAATTCGCCGATTTGTTTAAGTTAAATTCGAATAAATTTGAAATTAAGTGACCAAA	3243
QY	3252	ATAATTCGTGATTTGTTTAAAGTTAAATACGTAACAAATTTGAAATTAAGTATGATCA	3311
DB	3244	CCATCAG-----A-CA-----TGG--CGAT--A--ATG-----	3265
QY	3312	CCATCAGGTGAGAGCAACACAGATCAGTTGGATTTGGAGCGAAGACATGTTGACAAC	3371
DB	3266	-AAGTGGAGTTGGGTCATGACGAATCATGCGCATGGCTTGATCAAAAAAGGTATGAAG	3324
QY	3372	GAACTGGAGCTGGGCGACGACGATCTCCGACGCGCTCATCAAGAAAGGGATCAAG	3431
DB	3325	GGGACACCCAGCTGGAGGTGCCATTTGGGATGGCATGGAGTTTACAGATACATGGCGAT	3384
QY	3432	GAGCAGACCACTGGAGGTGCCATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT	3491
DB	3385	ATGAAACAAACAAAGCCCAAGAAATCAAAATTCATAAACAACACAAAGATGATTGGAAC	3444
QY	3492	ATGAAGAACAAACAAAGCCCAAGAAATTCATAAACAACAAAGATGATTGGAAC	3551
DB	3445	TCATAAACCAACAAAGATGAGTGGAAATGAGTGGAAATGAGTGGAAATGAGTGGAAAT	3504
QY	3552	TCATAAACCAACAAAGATGAGTGGAAATGAGTGGAAATGAGTGGAAATGAGTGGAAAT	3611
DB	3505	CAGACCATGACACTGCCAGCATTAATCTATATGTTAGCCATAAGAAATGACCATTCAG	3564
QY	3612	CAGACCATGACACTGCCAGCATTAATCTATATGTTAGCCATAAGAAATGACCATTCAG	3671
DB	3565	GACGAGAGCCAAAGGAGCGGAGACCATCGAGGCGAGGAGAAACCGACGCTCAG	3624
QY	3672	GACGAGAGCCAAAGGAGCGGAGACCATCGAGGCGAGGAGAAACCGACGCTCAG	3731
DB	3625	AAAGAGGACCTCGGCTCGACGAGAACTGGAGGAGGAGGCGGAGGCGGATGAGGCGCAG	3684
QY	3732	AAAGAGGATTTAGTCTCGACGAGAACTGGAGGAGGAGGCGGAGGCGGATGAGGCGCAG	3791
DB	3685	CTGGATGTTGACATCATCTATGCTCCCAACAAACGACGAGATTAATCGACGACTATCG	3744
QY	3792	CTGGATGTTGACATCATCTATGCTCCCAACAAACGACGAGATTAATCGACGACTATCG	3848
DB	3745	GCGGACTGTTCCCGGACTCGTACTACAAAGTTTCGATCTTGGCCGCGGAGGAGGAC	3804
QY	3849	GCTGATGCTGCCGATTCGATCTATGAGAAATTCGATCTTGGCCGCGGAGGAGGAC	3908
DB	3805	TCGCCCTCTGCGAGGATGGGCAATTTAGCTGAAATTTTCAATTAATTTGAAAT	3864
QY	3909	TCGCCCTCTGCGAGGATGGGCAATTTAGCTGAAATTTTCAATTAATTTGAAAT	3968
DB	3865	AAATATTTGAAACCGCATTTATCATATGATTTTAAATGAGTACGTTAGCTTTGGCCTTA	3924
QY	3969	AAATATTTGAAACCGCATTTATCATATGATTTTAAATGAGTACGTTAGCTTTGGCCTTA	4028
DB	3925	GAAGATGTTATTTACCGCATCGACCTGTCAGGATATCTACTACTATGATGATGATGATG	3984
QY	4029	GAAGATGTTATTTACCGCATCGACCTGTCAGGATATCTACTACTATGATGATGATGATG	4088
DB	3985	ATATTTACGTTGATTTCTTTTGGAGATGTTGATCAAAATGTTGGCCCTGGGCTTTAAG	4044
QY	4089	ATATTTACGTTGATTTCTTTTGGAGATGTTGATCAAAATGTTGGCCCTGGGCTTTAAG	4148
DB	4045	GTCATCTTCAACCAATGCTGTTGTTGGCTGATTTCTGATGTCATGATGATGATGATG	4104
QY	4149	GTCATCTTCAACCAATGCTGTTGTTGGCTGATTTCTGATGTCATGATGATGATGATG	4208
DB	4105	AAATTTGGTTGGCTTTGGTTCGGCTTAAATGATATAGCCGTTTATAGATCAATCGCAC	4164
QY	4209	AAATTTGGTTGGCTTTGGTTCGGCTTAAATGATATAGCCGTTTATAGATCAATCGCAC	4268
DB	4165	CTGCGCGCTTAAAGGCAATTCGCTGCTCTCTATAGATGAGGAGGATGAAAGTTGCTG	4224
QY	4269	CTGCGCGCTTAAAGGCAATTCGCTGCTCTCTATAGATGAGGAGGATGAAAGTTGCTG	4328

Tue Oct 14 14:18:10 1997

CC FILING DATE: 530
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Timian, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6318 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC Sequence 6318 BP: 1712 A; 1347 C; 1597 G; 1662 T; 0 other:
Query Match 56.2%; Score 3662; DB 67; Length 6318;
Best Local Similarity 84.7%; Pred. No. 0.00e+00;
Matches 4979; Conservative 0; Mismatches 813; Indels 84; Gaps 21;
Db 151 ATACGATATGATGAGGAGGACGAGATGAAGTCCACGCGGATCCACACTTGACAG 210
Qy 207 ATCCGATATGATGAGGAGGACGAGATGAAGTCCACACCGGATCCACACTTGACAG 266
Db 211 GGTGTCCTATACCTGTTGCAATGAGGAGGAGTTCGCGCGGAAATGGGCTCCACTCCT 270
Qy 267 GGTGTCCTATACCTGTTGCAATGAGGAGGAGTTCGCGCGGAAATGGGCTCCACTCCT 326
Db 271 CTCGAGGATATCGATCCCTACTACAGTAAATGTAGTACATTTGTAGTAATTAAGTAAGGA 330
Qy 327 CTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTTGTAGTAAAGTAAGGA 386
Db 331 AAGGATATTTTCGTTTTCCTCCCAAGCAATGTGCTGCTCGATCCATTCATTCG 390
Qy 387 AAGGATATTTTCGTTTTCCTCCCAAGCAATGTGCTGCTCGATCCATTCATTCG 446
Db 391 ATACGTCGTGTACCATTTATATTTTATGATATTCCTGTTTTCCTGTTTATTCATTCAC 450
Qy 447 ATACGTCGTGTACCATTTATATTTTATGATATTCCTGTTTTCCTGTTTATTCATTCAC 506
Db 451 ACTATTCATTAATTTGATTTTAAATGATTAATGCGACAAACCCACGCTCGAATCCACA 510
Qy 507 ACTATTCATTAATTTGATTTTAAATGATTAATGCGACAAACCCACGCTCGAATCCACA 566
Db 511 GAGTGATATTCACCGGAATCTACATTTGAATAGCTGTTAAAGTATGACGAGGT 570
Qy 567 GAGTGATATTCACCGGAATCTACATTTGAATAGCTGTTAAAGTATGACGAGGT 626
Db 571 TTCATTTATGCGGTTTACGTATCTAGAGATGCAATGGAATGGCTGGACTTCGTAGTA 630
Qy 627 TTCATTTATGCGGTTTACGTATCTAGAGATGCAATGGAATGGCTGGACTTCGTAGTA 686
Db 631 ATAGCTTTAGCTTATGTGACCATGGGATAGATTTAGGTAATCTCGAGCTTTGAGAAC 690
Qy 687 ATAGCTTTAGCTTATGTGACCATGGGATAGATTTAGGTAATCTCGAGCTTTGAGAAC 746
Db 691 TTTAGGGTACGCGAGCTCTGAAACCGTAGCCATTCGCGAGCTCTGAAACCGCTTCG 750
Qy 747 TTTAGGGTACGCGAGCTCTGAAACCGTAGCCATTCGCGAGCTCTGAAACCGCTTCG 806
Db 751 GGTGTCGTCATTTGATCTGTAATAAATCTACGCGATGTGATTAATTTGACATGTTTTC 810
Qy 807 GGTGTCGTCATTTGATCTGTAATAAATCTACGCGATGTGATTAATTTGACATGTTTTC 866
Db 811 CTGTCGGTGTTCGCGTATGGGCTTACAAATCTATATGGGTGTTCTTAAACAAAGTGC 870
Qy 867 CTGTCGGTGTTCGCGTATGGGCTTACAAATCTATATGGGTGTTCTTAAACAAAGTGC 926
Db 871 ATTAAAGGATTCCTCCTGACGCGAGTGGGGCAATCTGACCGATGAAATGTTTCTTA 930
Qy 927 ATCAAGAGTTCCTCGTGGCGGTTCCCTGGGCAATCTGACCGAGAGACTGGGACTAT 986

Db 931 CACAATAGCAACAGTTCCAAATGGTTTACGAGAACGATGCGAGTCATATCCGTTGTC 990
Qy 987 CACAATGCAATAGCTCCAAATGGTTTACGAGAACGATGCGAGTCATATCCGTTGTC 1046
Db 991 GGAATGATATCGGTGCGGCAATGCGGAGGATACGTCCTCGAGGGTTCGGC 1050
Qy 1047 GGAATGATATCGGTGCGGCAATGCGGAGGATACGTCCTCGAGGGTTCGGT 1106
Db 1051 CCAATCCCAACTACGACTACACAGTTTCGATTCATTCGTTGGCTTTCTGTCGCG 1110
Qy 1107 CCAATCCCAACTACGACTACACAGTTTCGATTCATTCGTTGGCTTTCTGTCGCG 1166
Db 1111 TTCGTCCTCATGACCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGCTGCAACAGCT 1170
Qy 1167 TTCGTCCTCATGACCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGCTGCAACAGCT 1226
Db 1171 GGACCTGCGACATGTTGTTTATAGTCATCATCTTCTAGGTTTCATTCATCTTGT 1230
Qy 1227 GGACCTGCGACATGTTGTTTATAGTCATCATCTTCTAGGTTTCATTCATCTTGT 1286
Db 1231 AATTGATTTGGCCATTTGTCATGCTCTTATGACGAATTCAAAGAGGCGGAGAA 1290
Qy 1287 AATTGATTTGGCCATTTGTCATGCTCTTATGACGAATTCAAAGAGGCGGAGAA 1346
Db 1291 GAAGAGGCTGCGGAGGAGGCGGATACGAGAGCTGAAGAGCGGAGCGCAGCAGCG 1350
Qy 1347 GAAGAGGCTGCGGAGGAGGCGGATACGAGAGCTGAAGAGCGGAGCGCAGCAGCG 1406
Db 1351 GCAAACTGGAGGAGGCGGCAATGTAGCAGCTCAAGCGCTCAGGATGCGAGGATGCC 1410
Qy 1407 GCAAACTGGAGGAGGCGGCAATGTAGCAGCTCAAGCGCTCAGGATGCGAGGATGCC 1466
Db 1411 GTCGCGGAGCTCTGATCCCGAGATGGCAAGAGTCCGAGTCTCTTCATTCATCTAT 1470
Qy 1467 GAAGAGGCTGCACTGCTATCCGGAATGGCAAGAGTCCGAGTCTCTTCATTCATCTAT 1526
Db 1471 GAAGAGGCTGCACTGCTATCCGGAATGGCAAGAGTCCGAGTCTCTTCATTCATCTAT 1530
Qy 1527 GAAGAGGCTGCACTGCTATCCGGAATGGCAAGAGTCCGAGTCTCTTCATTCATCTAT 1586
Db 1531 CGCAGCGTCGAAAGTGGAAATCGGAGTGGTGGTGTATACAAAGACACACGACCTACC 1590
Qy 1587 CGCAGCGTCGAAAGTGGAAATCGGAGTGGTGGTGTATACAAAGACACACGACCTACC 1646
Db 1591 ACAGCAC-CC--GCTACTAAAGTCCGTCAGGTTAGCAGACTTCCTTATCTTACCTGGT 1647
Qy 1647 ACAGCACACCAAGCTACCAAGTTGTAAGTGAAGAGCAGCATCTTATCTTACCTGGT 1706
Db 1648 TCACCATTTAACTACGCGCGGATCAGTGTTCACACAGTACACATACGAATGG 1707
Qy 1707 TCACCATTTAACTACGCGCGGATCAGTGTTCACACAGTACACATACGAATGG 1766
Db 1708 CGTGGAGCTTTGGTATACGAGTACGATCGCAAGCCTTGTACTGCAACATATCAG 1767
Qy 1767 CGTGGAGCTTTGGTATACGAGTACGATCGCAAGCCTTGTACTGCAACATATCAG 1826
Db 1768 GATCCAGCAGCAGCTTTGCCCTATGCCGATGACTCGAATGCGGTACACCATGTCGAA 1827
Qy 1827 GATCCAGCAGCAGCTTTGCCCTATGCCGATGACTCGAATGCGGTACACCATGTCGAA 1886
Db 1828 GAGAAATGGTGGCTATGATACGAGCTTACTTATGTAATTTAGGTTCTAGACATTTCTCA 1887
Qy 1887 GAGAAATGGTGGCTATGATGAGCTTACTTATGTAATTTAGGTTCTAGACATTTCTCA 1946
Db 1888 TATACCTCGCATCAATCAAGAAATCTCGTATACATCAGATGGTGTATTTGGTGGCATG 1947
Qy 1947 TATACCTCGCATCAATCAAGAAATCTCGTATACATCAGATGGTGTATTTGGTGGCATG 2006
Db 1948 GCGGCGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2007
Qy 2007 GCGGCGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2066

Db	2008	AATCAATCAATCGGTCTCCACCAATCGTGGAGTAGTAGCGCTGGTGGTGGCTATCC	2067
Qy	2067	AATCAATCAGT--GG-GC-CCCAACCAATGGCGGCACCA---C--CTG-TC-TGGACA--CC	2114
Db	2068	GATGCCAATCACAAAGAACAAAGGATATGAATGGGTGACAGGATTATACAGACGAGCT	2127
Qy	2115	ANTCACAGTGC---GATCATCGGACTACGAATTTGCCCTGGAGTCGACGGACGAAGCT	2171
Db	2128	GGCAAAATAAACCACACACAAATCCTTTATTCGAGCCCGCTCCAAACTCAAAACAGTGGTA	2187
Qy	2172	GGCAAGATTAAACATCATGACAATCCTTTATCGAGCGCGTCCAGACACAAACGGTGGTT	2231
Db	2188	GACATGAAGAAGTGTATGTGCTTTAAATGATATCATTTGAACAAGCCGCTGTGTCGCATAGT	2247
Qy	2232	GATATGAAGAATGTATGTGCTCTGTAATGACATCATCGAACAGGCGCGTGTGTCGCACAGT	2291
Db	2248	CSGTCTAGTGAACGAGGTG-----AGGACGATGACGAGAGT	2283
Qy	2292	CGGCGAAGCGATCGCGGCTGTCCGCTTTACTATTTCCACAGAGGACGATGACGAGGAT	2351
Db	2284	GGTCCCAACATTCAAAGGACATCGCCCTCGAAATACATCCTTAAAGGACATCGAAATCTTTTGT	2343
Qy	2352	GGCGCCGCTTCAAGACACAGCACTCGAAGTAGTCCTCAAGGCATCGATGTGTTTGT	2411
Db	2344	GTATGGGACTGTGTTGGGTGGTGTAAAAATTCAGGAATGGGTGCTCTTTATTGTGTTTC	2403
Qy	2412	GTGTGGGACTGTGTCTGGGTTTGGTTGAAATTTACAGGATGGGTATCGCTCATCGTCTTC	2471
Db	2404	GATCCATTGCTGGAGCTCTTCATTACCTCTGTGTATTGTGGTCAATACGATGTTTATGGCC	2463
Qy	2472	GATCCCTCTGTGAGCTCTTTCATCAGCTGTGCATTTGGTCAACACGATGTTTCATGGCA	2531
Db	2464	ATGGATCATCACGACATGAATCCGGAATTAGAGAAGTGCCTGAAAAGTGGTAACTATTTC	2523
Qy	2532	ATGGATCACCCAGATATGAACAGNGATGGAACCGCTGCTCAAGAGTGGCACTATTTC	2591
Db	2524	TTACAGGCCACTTTTCGGATTCGAGCCAGCATGAACATGATGGCCATGAGCCGCAAGTAC	2583
Qy	2592	TTACGCCCACTTTGCCATCGAGGCCACCATGAAGCTAAATGGCCATGAGCCCCAAGTAC	2651
Db	2584	TACTTCCAGGAAGGCTTGGACATTTTCGATTTTCATTTATTTGGCTTGTCTCTGCTGGAA	2643
Qy	2652	TATTTCCAGGAGGCTTGGAAACATCTTCGACTTCATTTATGTTGGCCCTATCGCTATTGGAA	2711
Db	2644	TTGGGCTGAGGGGTCTCCAGGCGCTCTCGGTGTTGAGAAGTTTTTCGTTTCTCTCGTGTGA	2703
Qy	2712	CTGGGACTGAGGGGTCTCAGGGTCTGTCGGTATTGGCTTCTTTCGATTCGTCGGTGA	2771
Db	2704	TTCAAAATGSCAAAATCATGGCCCACTGAAATTTACTCATTTTCGATTATGGCCGGGACA	2763
Qy	2772	TTCAAACTGSCCAAGCTTTGGCCACACTTAATTTACTCAITTTTCGATTATGGGACGCACT	2831
Db	2764	ATGGGTGCATTTGGGTAACTGCACATTTTGACATTTTGGAATATCATCTTCATCCCTGCCGTG	2823
Qy	2832	ATGGCGCTTTTGGGTAACTGCATTTTGACTTTTCGATTATCATCTTTCATCTTTTTCGGGTG	2891
Db	2824	ATGGGAATGCAACTTTTTCGSAAGACCAATATTGACCACAAAGGATCGCTACAAAGACCAT	2883
Qy	2892	ATGGGAATGCACTGTTTCGGAAGAATTTATCAATGATCAAAAGGACCGCTTTCCGGATGGC	2951
Db	2884	GAATTCGCGGCTTGAATTTTCCACCGACTTCATGSCACAGCTTCATGATGTGTTCCCGAGTG	2943
Qy	2952	GACCTGCGGCTTGAACATTCACCGACTTTATGACACAGCTTCATGATGCTGTTCCCGGGTG	3011
Db	2944	CTGTGCGGAGAGTGGATCGAGTCCATGTGGGACTGCATGTATGTGGGGGATGTCAAGCTGT	3003
Qy	3012	CTCTGCGGGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGACGTGGCGCATGTCTCGTCG	3071
Db	3004	ATACCTTCTCTTGGCCAGGTCGTGATCGGCAATCTGTGGTCTTAACTTTTCTTAA	3063
Qy	3072	ATTCCCTTCTCTTGGCCACCGTGTGATCGGCAATCTGTGGTAACTTAACTTTTCTTAA	3131
Db	3064	GCCTTGTCTTTGTCCAACTTCGGTCTCATCTAGTCTTTATCAGCCCGGACTTCGCGCAATGAT	3123

QY	3132	GCCTTGTCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCGACTTCGGGATAAAGCAT	3191
DB	3124	ACCAATAAAATAGCAGAGGCGCTTCAATCGTATTGCTCGTGTAAAGAACTGGGTGAAACGT	3183
QY	3192	ACGAATAAATAGCCGAGCGCTTCAATCGAATGGCCGATTTAAAGTTGGGTTAAGCGT	3251
DB	3184	AATATTCCGATTTGTTTTAAGTTTAATTCGAAATAAATTTGACAAATCAAAATAGTGACAA	3243
QY	3252	AATATTGCTGTTTTCAGTTTAATACGTAACAAATTGACAAATCAAAATAGTGATCAA	3311
DB	3244	CCATCAG-----A-A-CA-----TGG--CGAT-A--ATG-----	3265
QY	3312	CCATCAGGTTGAGAGGACCAACAGATCAGTTTGGGCGAAGAGCATGGTGCAAC	3371
DB	3266	-AACTGGAGTTGGGTATGACGAAATCATTGGCGATGCGCTTGATCAAAAGGGTATGAAG	3324
QY	3372	GAACTGGAGCTGGCCACGACGAGATCTTCGCCGAGGCCCTCATCAGAAGGGGATCAAG	3431
DB	3325	GGCGAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGAGTTTCACGATACATGGCGAT	3384
QY	3432	GAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATTCAGCATACACGGCGAC	3491
DB	3385	ATGAAAACACAAAGCCCAAGAAATCAAATTTCAATAAACACACAAACGATGATTGGAAC	3444
QY	3492	ATGAAGAACAACAGCCGGAAGAAATCCAATATCTAAATTAACGCAACGATGATTGGCAAC	3551
DB	3445	TCATAAACCAACCAAGACATACACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATA	3504
QY	3552	TCATTTAACCCACCAAGACAATAGACTGGAAACAGAGCTTAACCATAGAGGTTTGTCTTTA	3611
DB	3505	CAGGACGATGACACTGCCAGCATTAACCTCATATGTTAGCCATAAAGAAATCGACCATCAAG	3564
QY	3612	CAGGACGACGACTGCCAGCAATTAACCTCATATGTTAGCCATAAAGAAATCGACCATCAAG	3671
DB	3565	GACGAGACCAAAAGGCGCGCGAGACCATCGAGGGCGAGGAGGAGAAACGCGAGTCAAG	3624
QY	3672	GACGAGAGCCACAAGGCGCGCGAGAGCGATGGAGGGCGAGGAGAAACGCGAGCGCCAGC	3731
DB	3625	AAAGAGGACCTTCGGCTTCGACGAGGAACCTGGACGAGGAGGCCGGAGGGGATTAAGGGCCAG	3684
QY	3732	AAGGAGGATTTAGCTCTCGACGAGGAACCTGGACGAGGAGGGGGAATGCGAGAGGGCCCG	3791
DB	3685	CTGGATGGTGACATCATCTATTCGCCAAAACGACGACGAGATTAATCGACGACTATCCG	3744
QY	3792	CTCGACGGTGATATCATTTATTCATGCACA--CGACGAGGATATACTCGATGAATATCCA	3848
DB	3745	GCGGACTGTTTTCCCGACTCGTACTACAAGAAGTTTCGGATCTTGGCGCGGACGAGGAC	3804
QY	3849	GCTGATTGCTGCCCGATTCTGTAATAAGAAATTTCCGATCTTAAGACGGTGACGATGAC	3908
DB	3805	TCGCGGTTCTGGCAAGATGGGCAATTTACGACTGAAAACCTTTTCAATTAATTGAAAT	3864
QY	3909	TCGCGGTTCTGGCAAGATGGGCAATTTACGACTGAAAACCTTTTCAATTAATTGAAAT	3968
DB	3865	AAATATTTGAAACCGCAGTTATCACTATGATTTAATGAGTAGCTTAGCTTTGGCCCTTA	3924
QY	3969	AAATATTTGAAACAGCTGTATCACTATGATTTAATGAGTAGCTTAGCTTTGGCATTA	4028
DB	3925	GAAAGATTTCATTTACCCGATCGACCTGTCATCGCAGGATATATTTGTAATACATGGACAG	3984
QY	4029	GAAAGATTTCATCTGCCACAAGACCCACTGCAAGGATATTTTACTATATGACAGACA	4088
DB	3985	ATATTACGGTGATATCTTTTTGGAGATGTTGATCAATGGTTGGCCCTGGGCTTTAAG	4044
QY	4089	ATATTACGGTTATTTCTTTTGGAAATGTTAATCAAGTGGTTGGCCCTCGGCTTCAAA	4148
DB	4045	GTTTACTTCACCAATGCTGGTGTGGCTGGATTTTCGTTGATGTGTCATGTCATCGCTTATA	4104
QY	4149	GTTTACTTCACCAACGCGTGGTGTGGCTCGATTTGCTGATTTGTCATGGTATCGCTTATC	4208
DB	4105	AATTTGGTTGCGGTTTGGTCGGGCTTTAAATGATATAGCCGTGTTTATGATCAATCGCACA	4164

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QY 4209 AACTTGGTTCCTTCACTTGTGGAGCTGGTGTATTAAGCCTTCAAGACTATCGGACG 4268
 Db 4165 CTGCGCGCTTAAGGCAATTTGGTGTCTCTAGATGGGAGGTATGAAGATGTTGCTG 4224
 QY 4269 TTAAGAGCACTGAGACCACTAGTGCCATGTCCTGATATGAGGAGTATGAGGTCGTT 4328
 Db 4225 AATGCGCTGGTTCAGCACTATACCGTCCATCTTCAATGTGCTATGCTGTGCTGATATT 4284
 QY 4329 AATGCGCTGTACAACTATACCGTCCATCTTCAATGTGCTATGCTGTGCTGATATT 4388
 Db 4285 TGGCTTATTTTGGCAATTAAGGAGTACAGCTTTTGGTGGAAATATTTTAAGTGTAAA 4344
 QY 4389 TGGCTTATTTTGGCAATTAAGGAGTACAGCTTTTGGTGGAAATATTTTAAGTGTAAA 4448
 Db 4345 GATGGAATGACACTGTGCTGAGCGATGAATCATACCGAATCGTAATCGTCCGAAAGT 4404
 QY 4449 GACATGAATGACAGCAAGCTCAGCGAGATCATACCAATCGCAATGCCCTGCGAGAGC 4508
 Db 4405 GAAACTACACTGGGAAATTCGGCAATGAACCTTCGATCATGTAGTAAATGCTATCTC 4464
 QY 4509 GAGAACTACACTGGGGAATTCAGCAATGAATTCGATCATGTAGTAAATGCTATCTC 4568
 Db 4465 TGTCTATTTTCAAGTGGCCACTTTAAGGCTGGATCCAGATTTATGACGATGCTATGAT 4524
 QY 4569 TGCCTTTTCAAGTGGCCACTTTAAGGCTGGATCCAGATTTATGACGATGCTATGAT 4628
 Db 4525 TCACGAGGTTGGAACAGCAAGCAATTCGTAACGAACTATCATGTATTTATATTC 4584
 QY 4629 TCACGAGGTTGGAACAGCAAGCAATTCGTAACGAACTATCATGTATTTATATTC 4688
 Db 4585 GTATTTCTCATATATTTGGATCATTTTTCACACTCAATCTGTTTCATGTTTATCAT 4644
 QY 4689 GTATTTCTCATATATTTGGATCATTTTTCACACTCAATCTGTTTCATGTTTATCAT 4748
 Db 4645 GATAATTTTAAAGCAAGCAAGCAAGCAAGTGTGATCATTTAGAAATGTTTCATGACAAA 4704
 QY 4749 GATAATTTTAAAGCAAGCAAGCAAGCAAGTGTGATCATTTAGAAATGTTTCATGACAAA 4808
 Db 4705 GATCAGAAAAGTACTATTAATGCTATGAAAAGTGGCTTAAACCACTTAAAGCC 4764
 QY 4809 GATCAGAAAAGTACTATTAATGCTATGAAAAGTGGCTTAAACCACTTAAAGCC 4868
 Db 4765 ATTCAGAGCGGAGTGGGAGCAAGCAAGCAAGTGTGATCATTTAGAAATGTTTCATGACAAA 4824
 QY 4869 ATTCAGAGCGGAGTGGGAGCAAGCAAGCAAGTGTGATCATTTAGAAATGTTTCATGACAAA 4928
 Db 4825 TTCGATATAATCATTTATTTGTTTCATGTTTAAACATGTTTACCATGACCTCGATCGG 4884
 QY 4929 TTCGATATAATCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4988
 Db 4895 TACGACGCTCCGAGGCGTACAACTATCTCGCAAACTCAATGGGATATTCGTAGTT 4944
 QY 4989 TACGATGCTGGGACAGTATACCGGCTCTAGACTATCTCAATCGGATATTCGTAGTT 5048
 Db 4945 ATTTTCAGTGGCAATGCTATTTAAATAATTTGCTTTAGCATATCAGTATTTCAAGAG 5004
 QY 5049 ATTTTCAGTGGCAATGCTATTTAAATAATTTGCTTTAGCATATCAGTATTTATGAG 5108
 Db 5005 CCATGGAATTTATTTAGTATGATGTTGCTATTTTATCCATCTTAGTCTTTGCTAGTACG 5064
 QY 5109 CCATGGAATTTATTTAGTATGATGTTGCTATTTTATCCATCTTAGTCTTTGCTAGTACG 5168
 Db 5065 GACATCATGGAAGTATTTGCTATCGCCGACATGCTCGGTGGTGGAGTGGCCAAA 5124
 QY 5169 GATATTTTCGAGAACTACTTGGTGTGCGGAGCTGCTCGGAGTGGTGGGCGGAAA 5228
 Db 5125 GTGGGTGCTGCTCGGTTTATGCTAGGAGTGCAGAGGTATCCGAGGTGCTGCTGCTGCG 5184
 QY 5229 GTGGGCGGTGCTTTCGACTGTTGAGGAGGAGGCAAGGCAATTCGACACTGCTCTTCGCG 5288
 Db 5185 TTAGCCATGCTGCTGCTGCTGCTTATTCACAAATTTGCTGCTGCTGCTGCTGCTGCTGCT 5244
 QY 5289 TTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5348

Db 5245 ATCTTTGTATCTTTTGGCATGCTCTTCTTCTCATGATCTCAAGAGAGAGCGGCATAAAT 5304
 QY 5349 ATCTTTGCCATTTTGGCATGCTCTTCTTCTCATGATCTCAAGAGAGAGCGGCATAAAT 5408
 Db 5305 GCTGTGTATTAATTTAAGACATTTTGGCAGAGTATGATATTTGCTTTTTCAGATGCTTACC 5364
 QY 5409 GAGCTCTACACTTCAAGACCTTTTGGCCAGAGCATGCTCTGCTCTTTTCAGATGCTGACG 5468
 Db 5365 TCAGCCGGTTGGGATGGTGTGTAGATGCCATTTATCAATGAGGAGAGATTTGGATTCACACC 5424
 QY 5469 TCAGCCGGTTGGGATGGTGTGTAGATGCCATTTATCAATGAGGAGAGATTTGGATTCACACC 5528
 Db 5425 GACAACGAGCAAGGCTATCCGGCAATTTGCTTCCAGGAGTGTATATATGCTATGCTTCTC 5484
 QY 5529 GACAGCGCAAGAGGCTATCCGGCAATTTGCTTCCAGGAGTGTATATATGCTATGCTTCTC 5588
 Db 5485 CTCTCATATCTAGTATTAAGCTTTTGTATGATGATTTATATATGCTATGCTTCTC 5544
 QY 5589 CTCTCATATCTAGTATTAAGCTTTTGTATGATGATTTATATATGCTATGCTTCTC 5648
 Db 5545 GAGNACTATAGCCAGCTACGGAGGATGTACAGAGGCTTCCACGAGAGATTTACGAT 5604
 QY 5649 GAGAACTATATAGTACGGCCAGGAGGCTGCAAGAGGCTTAACGAGAGGAGTACGAC 5708
 Db 5605 ATGTACTACGAGATTTGGCAACAATTTGATCCCGAGGCGGAGGAGTACGATCCAGGCGGAGAG 5664
 QY 5709 ATGTACTATGAGATCTGGCAACAATTTGATCCCGAGGCGGAGGAGTACGATCCAGGCGGAGAG 5768
 Db 5665 CAGTGTGCGGATTTTGGAGGCTGCGGAGGCGGAGGAGTACGATCCAGGCGGAGAGAG 5824
 QY 5769 CAGTGTGCGGATTTTGGAGGCTGCGGAGGCGGAGGAGTACGATCCAGGCGGAGAGAG 5888
 Db 5725 TACAAATATCATATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 5784
 QY 5829 TACAAATATCATATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 5888
 Db 5785 ATATTGGATGCTTCCAGCAAGGAGTCTTTCGCGGAGGAGTATCCGATTCGAGGAGAGC 5844
 QY 5889 ATCTTCGAGCGGCTTACGAAAGACTTCTTTCGCGGAGGAGTATCCGATTCGAGGAGAGC 5948
 Db 5845 GGTGAAATTTGTGAGATGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5904
 QY 5949 GGTGAGATTTGTGAGATGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6008
 Db 5905 ACAGTGTGCGGCGGAGTGGAGGAGTACGCGCAAGGCTGCGCAAGGAGTATCCGATTCGAGGAGAGC 5960
 QY 6009 ACAGTGTGCGGCGGAGTGGAGGAGTACGCGCGGCTAATCCAGAGGAGGAGGAGGAGGAGGAGGAG 6064

RESULT 9
 ID US-08-608-618-2 STANDARD; DNA; UNC; 6318 BP.

AC XXXXX
 DT Sequence 2, Application US/08608618.
 DE Sequence 2, Application US/08608618.
 CC GENERAL INFORMATION:
 CC APPLICANT: Soderlund, David M.
 CC APPLICANT: Ingles, Patricia J.
 CC APPLICANT: Ingles, Patricia J.
 CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
 CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
 CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
 CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
 CC NUMBER OF SEQUENCES: 19
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Nixon, Hargrave, Devans & Doyle LLP
 CC STREET: P.O. Box 1051, Clinton Square
 CC CITY: Rochester
 CC STATE: New York
 CC COUNTRY: USA
 CC ZIP: 14603
 CC COMPUTER READABLE FORM: Floppy disk
 CC MEDIUM TYPE: Floppy disk

CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/608,618
CC	FILING DATE:	
CC	CLASSIFICATION:	530
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Timian, Susan J.
CC	REGISTRATION NUMBER:	34,103
CC	REFERENCE/DOCKET NUMBER:	19603/600 (CRF D-1657)
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	716-263-1636
CC	TELEFAX:	716-263-1600
CC	INFORMATION FOR SEQ ID NO:	2:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	6318 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	cDNA
CC	Sequence	6318 BP; 1713 A; 1349 C; 1592 G; 1664 T; 0 other;
SC		
	Query Match	56.28; Score 3660; DB 67; Length 6318;
	Best Local Similarity	84.78; Pred. No. 0.00e+00;
	Matches	4978; Conservative 0; Mismatches 814; Indels 84; Gaps 21;
Dbb	151	ATACGATATCATCAGCAGGACGAAGATGAAGGTCCACAGCGGATCCCACACTTGAACAG 210
QY	207	ATCCGATATGATCAGCAGGACGAGGATGAAGGTCCACACCGGATCTACACTTTGAACAG 266
Dbb	211	GGTGTCCTATACCTGTTCGAAATGCAGGCGAGCTTCCGCCGGGAATTGGCCTCCACTCCT 270
QY	267	GGTGTCCAATACCCTGTTCGATTGCAGGCGAGCTTCCGCCGGGAATTGGCCTCCACTCCT 326
Dbb	271	CTCGAGGATATCGATCCCTTCTCACAGTAATGTACTGACATTTCTAGTATAAAGTAAGA 330
QY	327	CTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTCCTAGTTGTGAAGCAAAGA 386
Dbb	331	AAGGATATTTTTCGTTTTCTGCTCAAAAAGCAATGGCTGCTCGATCCACTCAATCCG 390
QY	387	AAAGATATTTTTTCGTTTTCTGATCANAAAGCAATGGGATGCTCGATCCACTCAATCCG 446
Dbb	391	ATACGTCGTGTAGCCATTTATATTTTAGTCATCCCTTGTTTTCGTTATTCATTATCAC 450
QY	447	ATACGTCGTGTGCCATTTACATTTCTAGTGCATCCATTAATTTTCCCTATTTCATCATCAC 506
Dbb	451	ACTATCTAACTAATGTATTTTAAAGTAAATCGGNACAACGCCACGGCTCGAATCCACA 510
QY	507	ACAATTTCTCGTCAACTGCATCTCTGATGATTAATCCGACAACGCCACGGTTGAGTCCACT 566
Dbb	511	GAGTGATATTTACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT 570
QY	567	GAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT 626
Dbb	571	TTCAATTTATGCCCGTTTACGTATCTTAGAGATGCATGGAAATTTGGCTGGACTTCGTAGTA 630
QY	627	TTCAATTTATGCCCGTTTACGTATCTTAGAGATGCATGGAAATTTGGCTGGACTTCGTAGTA 686
Dbb	631	ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTGAATCTCGGAGCTTTGAGAACA 690
QY	687	ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGTGAATCTTAGAGATGCATGGAAAT 746
Dbb	691	TTTAGGGTACTCGGAGCTCTGAACCGGTAGCCATTTGTCGAGGTCTAAACACCATGTG 750
QY	747	TTTAGGGTGTGCGAGCGCTTAAACCGGTAGCCATTTGTCGAGGTCTGAAGACCATCGTC 806
Dbb	751	GGTGCTCTCATTTGAATCTGTAAAAAATCTACGGGATGTGATAATTTTGACAATGTTTTCC 810
QY	807	GGCGCGCTCATCGNAICGGTGAAGATCTCGCGGATGTGATTTATCTGACCATGTTCTCC 866
Dbb	811	CTGTGCGTGTTCGCGTGTATGGCCCTACAAATCTATATGGGTGTTCTTAACACAAAAGTGC 870

Qy	867	CTGTCCGGTGTTCGGTTGTGATGGCCCTACAGATCTATATGGCGGTGCTCTACCGAGAAGTGC	926
Db	871	ATTAAACGATTTCCTCCCTGGACGCGCAGTTTGGGCAATCTGACCGATGAAGAACTGTTTCTA	930
Qy	927	ATCAAGAAGTTCCCGCTGGACGGTTCCCTGGGCAATCTGACCGACGAGAACTGGGACTAT	986
Db	931	CACAATAGCAACAGTTTCCAAATTTGCTTACGGAGAACGATGGCGAGTCAATATCCGGTGTGC	990
Qy	987	CACAAATCGCAATAGTCCAAATTTGGTATTCCGAGGACGAGGCGATCTCATTTTCCGTTATGC	1046
Db	991	GGGAATGTATCCGGTCCGGGCAACATCGCGGAAGATTACGTCTGCCTGACGGGCTTCGGC	1050
Qy	1047	GGCAATATATCCCGTGGGGGCAATCGGACGAGATACGTGTGGCTCGAGGGGTTTGGT	1106
Db	1051	CCCAATCCCAACTACGACTACACAGTTTCGACTCATTTCCGTTGGGCTTTCCTGTCGGCG	1110
Qy	1107	CCGAATCCGAATTTATGCTACACAGCTTCGATTCTGTTCCGATGGCTTTCCTGTCCGCC	1166
Db	1111	TTTGGTCTCATGACCAAGATTTCCTGGGAGGATCTGTATCAGCAGCTGCTCTCAAGCAGCT	1170
Qy	1167	TTCCGGTGTATGACACAGGACTTCTGGAGGATCTGTACCAGCTGGTGTTCGCGCGCGCC	1226
Db	1171	GGACCTTGGCACATGTTGTCTTTATAGTATCATCTTCCCTAGGTTTCATCTATCTTTGTG	1230
Qy	1227	GGACATTTGGCACATGCTGTCTTTATAGTATCATCTTCCCTAGGTTTCATCTATCTTTGTG	1286
Db	1231	AAATTGATTTTGGCCATTGTGCCATGTCCTTATGACGAATTGCAAAAGAAGCCGCAAGAA	1290
Qy	1287	AAATTGATTTTGGCCATTGTGCCATGTCGTATGACGAATTGCAAAAGAAGCCGCAAGAA	1346
Db	1291	GAAGAGCTGCCGAGGAGGAGCGGATTCGAGAAAGCTGAAGAAGCGGCGAGCAAGCGCG	1350
Qy	1347	GAAGAGCTGCCGAGGAGGAGCGGATACCTGAAGCGGAAGAGCTGCGCGCCGCCAAGAG	1406
Db	1351	GCCAACTGAGGAGCGGGCCCAATGTAGCAGCTCAAGCGGCTCAGGATGCAAGCGGATGCC	1410
Qy	1407	GCCAACTGAGGAGCGGGCCCAATGGCGAGGCTCAGGAGCAGCGGATGCGGCTGCGCGCC	1466
Db	1411	GCTCGGCAGCTCTGCATCCGAGATGGCAAGAGTGCACAGTCTCTGTGATTAGCTAT	1470
Qy	1467	GAAGAGCTGCATGCTATCCGGAATGGCCAGAGAGTTCGACGATTTCTTGCATCAGCTAT	1526
Db	1471	GAATGTTTGTTCGGCGGAGAGGCAACGATGACAAACAAAGGAGAGAGATGTCGATA	1530
Qy	1527	GAGCTATTTTGGCGCGAGAGGCAACGATGACAAACAAAGAGAGAGATGTCGATA	1586
Db	1531	CGCAGCTCGAAGTGAATCGGAGTCGGTGGAGCTTATCAAGAGCACACGACCACTTACC	1590
Qy	1587	CGGAGCTCGAGGTGAGTCTGGAGTCGGTGGAGCTTATCAAGAGCACACGACCACTTACC	1646
Db	1591	ACAGCAC-CC--GCTACTAAAGTCCGTCAAGTTAGCAGACTTCCCTTATCCCTTACCTGGT	1647
Qy	1647	ACAGCACCAACGCTACCAAGTTCGTAAGTGGACGACATCCTTATCCTTACCTGGT	1706
Db	1648	TCACCATTTAACCTACGCGGGGATCACGTAGTTTACACAAAGTACACAATACGAAATGGG	1707
Qy	1707	TCACCGTTTAACTACGCGGGGATCACGTAGTTTACACAAAGTACACAATACGAAATGGG	1766
Db	1708	CGTGGAGCTTTTGGTATACGAGTACGATCCGAGCCATTTGGTACTCGAAACATATCAG	1767
Qy	1767	CGTGGCGCTTTTGGTATACCGGTACGATCTGTAAGCCATTTGGTATTTGTCAAACATATCAG	1826
Db	1768	GATGCCCAGCAGCATTTGGCCTATGCCGATGACTCGAATCGCGTAACCACTATGTCGAA	1827
Qy	1827	GATGCCCAGCAGCATTTGGCCTATGCCGAGACTCGAATCGCGTACCCCGGATGTCGAA	1886
Db	1828	GAGAATGGTGCCATTATAGTACCAGGCTACTATTGTAATTTAGGTTCTTAGACATTTCTCA	1887
Qy	1887	GAGAAATGGGCGCATATAGTCCCGTGTACTATGGCAATCTAGGCTCCCGACATCATCG	1946
Db	1888	TATACCTTCGCATCAATCAAGATCTCGTATATACATCACATGTTGATTTATGGTGGCATG	1947
Qy	1947	TATACCTTCGCATCAATCAAGATCTCGTATATACATCACATGTTGATTTATGGTGGCATG	2006

D	b	1948	GCGCCATGGGTGCGCAGCAAAATGACCAAGAGACAATTGCCAGTGCACACACGC	2007
Q	y	2007	GCGTCATGGCGCTCAGCAAAATGACCAGGAGACAATTGCGAACCGCACACACGC	2066
D	b	2008	AATCAATCAATCGTGCTGCACCAATGTTGGTGTAGTACGCGCGGTGGTGGGTATCCC	2067
Q	y	2067	AATCAATCAAT - GG - GC - GCCACCAATGGCGCACAC - CTGTC - TGGGA - C - A - CC	2114
D	b	2068	GATGCCAATCACAGGACAAGAGGATTAATAATGGGTGACGATATACAGACCAAGCT	2127
Q	y	2115	AATCACAAGCTC --- GATCATCGGACTAGCAAATTTGGCTGGGTGACGACGAGCT	2171
D	b	2128	GGCAAAATTAACACACACAGCAATCTTTTTATCGACCGCGTCCAACACTCAACAGTGTGA	2187
Q	y	2172	GGCAAGATTAACACATCATGACATCTCTTTTATCGAGCCGCTTCAGACACAAAACGGTGT	2231
D	b	2188	GACATGAAGAATGTTATGGTCTTAATATGATATCATTTGAACAAGCCGCTGGTGGCATAGT	2247
Q	y	2232	GATATGAAGAATGTTATGGTCTGCTGAATGACATCATGACAGAGCCGCTGGTGGCACAGT	2291
D	b	2248	CCTGCTAGTAGACAGTG --- AGGACGATGACGAAGAT	2283
Q	y	2292	CGGCAAGCGATCGCGGTGCTCTCGTTACTATTTCCACAGAGGACGATGACGAGAT	2351
D	b	2284	GGTCCACATTAACAGGACATCGCCCTCGAATATATCTATAAAGCATCGAAATCTTTGT	2343
Q	y	2352	GGCGGACGTTCAAAGACAAGGACATCGAAGTGATCTCAAAGGACATCGATGTTGT	2411
D	b	2344	GATGGGACTGTTGTTGGTGTGGTGTAAATTTACAGAAATGGTCTCTTTATTTGTTTC	2403
Q	y	2412	GTTGGGACTGTTGTTGGTGTGGTGTAAATTTACAGAGTGGTATCGCTCATCGTCTTC	2471
D	b	2404	GATPCCATCGTGGAGCTCTTCATTAACCTGTGATTTGGTCAATACAAATGTTTCATGGCC	2463
Q	y	2472	GATCCCTCGTGGAGCTCTTCATCGCTGTGATTTGGTCAACACAGATGTTTCATGGCA	2531
D	b	2464	ATGGATCATCAGACATGAATCCGAATTAGAAGAGTGTCTGAAAGTGGTAACTATTTTC	2523
Q	y	2532	ATGGATCATCAGACATGAATGAACAGGATGGAACGCTGCTCAAGAGTGGCAACTATTTTC	2591
D	b	2524	TTCACGCCACTTTTGCATTTAGGCGACGATGAACACTGATGGCCATGAGCCCGCAAGTAC	2583
Q	y	2592	TTCACGCCACTTTTGCATTCGAGGCGACCATGAAGCTAATGGCCATGAGCCCGCAAGTAC	2651
D	b	2584	TACTTCAGNAGGCTGGAACATTTTCGATTTTCATTTATTTGGTCTGCTGCTGGA	2643
Q	y	2652	TATTTCCAGAGGCTGGAACATTTTCGATTTTCATTTATTTGGTCTGCTGCTGGA	2711
D	b	2644	TTGGGCTTGGAGGTGTCCAGGCGCTGCGGTGTGAGAGTGTGCTGCTGCTGCTGTA	2703
Q	y	2712	CTGGGACTCGAGGTGTCCAGGCTGTGCGGTATTCGTTTTCGATTTGCTGGTGTGA	2771
D	b	2704	TTCAAATGGCAAAATCATGCCCCACACTCAATTTACTCATTTTCGATTTAGGCGCGACA	2763
Q	y	2772	TTCAAATGGCAAGCTGTGCCCCACACTCAATTTACTCATTTTCGATTTAGGAGCACAC	2831
D	b	2764	ATGGGTGATTTGGGTAAATCTGACATTTGTTGTTGATTAATCATCTTCATCTTTGGCGGT	2823
Q	y	2832	ATGGGCGTTTGGGTAAATCTGACATTTGTTGTTGATTAATCATCTTCATCTTTGGCGGT	2891
D	b	2824	ATGGGAATGCAACTTTTCGAAAGAACTATATTGACCACAGGATCGCTTCAAGGACCAT	2883
Q	y	2892	ATGGGAATGCAACTTTTCGAAAGAACTATATCATGATCAGAGGACCGCTTTCGGGATGGC	2951
D	b	2884	GAATTAACCGCTGGAACCTTACCGACCTTCATGNCAGCTTCATGATTTGTTCCGAGTG	2943
Q	y	2952	GACCTGCCGCTGGAACCTTACCGACCTTATGACAGCTTCATGATTCGTTCCGGGTG	3011
D	b	2944	CTGTGGGAGGTGGATCGAGTCCATGTGGGACTGCATGTATGTGGGCGATGTCAGCTGT	3003
Q	y	3012	CTGTGGGAGATGGATCGAGTCCATGTGGGACTGCATGTAGTGGGCGATGTCCTGTGC	3071

4149 GTGACTTCAACAACGGGTGGTGGCTCGATTTCGTGATGTGATGCTATC 4208
4105 AATTGGTGGCGTGGTGGCGCTTAATGATATAGCCGTTTAGATCAATCGGCACA 4164
4209 AACTTCGTGGTTCACATTTGGTGGAGCTGGTGGTATTCGAAGCCCTCAAGACTATCGGAAC 4268
4165 CTGGCGCCCTTAAGCCATTCGGTGGCTGCTCTAGATGGGAGGTATGAAGTGTGGTG 4224
4269 TTAAGACACTGAGACCACTACGTGCCATGTCCGATATGACGGCATGAGGGTGGTGGT 4328
4225 AATGGCTGGTCAAGCTATACCTGCCATCTTCAATGCTATGATGCTGCTGATATTT 4284
4329 AATGGCTGGTCAAGCTATACCTGCCATCTTCAATGCTATGATGCTGCTAATATTT 4388
4285 TGGCTATATTTTGGCATATATGGGAGTACAGCTTTTCTGCGAATATTTTAAGTGA 4344
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4345 GATGGTAAATGACACTGTCTGAGCCATGAAATCATACCGAATCGTAATGCTGCAAAAGT 4404
4449 GACATGAATGACCAAGCTCAGCCACGAGATCATACCAATCGCAATGCCCTGGAGAGC 4508
4405 GAAACTACACTGGGAAAATTCGGCAATGAACTTCGATCATGATGATGCTATCTC 4464
4509 GAGAACTACAGTGGGTGAATTCAGCAATGAATTTTCGATCATGATGATGCTATCTG 4568
4465 TGTCTATTTCAAGTGGCCACCTTTAAGGCTGGATCCAGATATTAAGATGCCATGAT 4524
4569 TGGCTTTTCCAAATGGCCACCTTTCAAGGCTGGATACAAATCATGAAGATGCTATCGAT 4628
4525 TCACGAGAGTGGACCAAGCAGCCGATCCGAGAAACCAATATCTACATGATATTTATTT 4584
4629 TCACGAGAGTGGACCAAGCAACCAATTCGTGAACGACATCTACATGATATTTATTT 4688
4585 GTATCTTCATATATTTGGATCATATTTTACACTCAATCTGTTTATGTTGTTATCAT 4644
4689 GTATCTTCATATATTTGGATCATATTTTACACTCAATCTGTTTATGTTGTTATCAT 4748
4645 GATATTTTAAATGAACAAAGCAAGCAAGCAGTGGATCATTTAGAAATGTTTCATGACAGAA 4704
4749 GATATTTTAAATGAACAAAGCAAGCAAGCAGTGGATCATTTAGAAATGTTTCATGACAGAA 4808
4705 GATCAGAAAAAGTACTATAATGCTATGAAAAGATGGGCTCTAAAAAACCACTTAAAGCC 4764
4809 GATCAGAAAAAGTACTATAATGCTATGAAAAGATGGGCTCTAAAAAACCACTTAAAGCC 4868
4765 ATTCAGACCGAGGTGGCGACCAAGCAATAGTATTCGAAATAGTTTACAGATAAAGAAA 4824
4869 ATTCAGACCAAGGTGGCGACCAAGCAATAGTATTCGAAATAGTTTACAGATAAAGAAA 4928
4825 TTCGATATAATCATATGTTGTTTCAATGGCTTAAACATGTTTACCATGACCCCTGATCGG 4884
4929 TTCGATATAATCATATGTTTCAATGGCTTAAACATGTTTACCATGACCCCTGATCGT 4988
4885 TACGACGCTCCGAGCGGTACAACTATCTCCGCAAACTCAATGGGATATTCGTAGTT 4944
4989 TACGATGCTCGGACACGTATACCGGTCTCTAGACTATCTCAATGCGATATTCGTAGTT 5048
4945 ATTTTCAGTGGCAATGCTATTAATAATATTCGTTTACGATATCATATTTTCAAGAG 5004
5049 ATTTTCAGTTCGGAATGCTATTAATAATATTCGTTTACGATATCATATTTTATTAG 5108
5005 CCATGGAATTTATTTGATGATGTTGCTCATTTTATTCATCTAGGTCCTGTTACTCAGC 5064
5109 CCATGGAATTTATTTGATGATGTTGCTCATTTTATCCATCTTAGGTCCTGTTACTTAGC 5168
5065 GACATCATGAGAAGTATTTGATTCGCGGACACTGCTCCGTTGGTGGAGAGTGGCCAAA 5124
5169 GATATATCAGAGAAGTACTTCTGTCGCGGACCTGCTCCGAGTGGTGGTGGCGAAA 5228
5125 GTGGTCTGCTCGCTTATGATCAAGGGTGGCAAGGGTATCCGAGACCTGCTGTTCCGC 5184

5229 GTGGCGCGTCTCTTCGACTGGTGAAGGAGCCAAAGGSCATTCGGACACTGCTCTTCGCG 5288
5185 TTAGCCATGCTGGTGGCTGCTTATCAACATTTGCTGTTGCTGTTGCTGGTGGTGGTTC 5244
5289 TTGGCCATGCTGGTGGCGCGCTTCAACATCTGCTGCTGCTGCTGCTGGTGGTGGTTC 5348
5245 ATCTTCTCATCTTTTGGGATGCTCCTTTCATGATGCTCAAGAGAGAGCGGATCAAT 5304
5349 ATCTTTCGCAATTTTCGCGATGCTGCTTCTCATGACCTGAAGGAGAGAGCGGATTAAC 5408
5305 GCTGCTGATATTTTAAGACATTTGGCCAAAGTATGATATGCTGTTTCAGATGCTCACC 5364
5409 GACGCTACAACTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTTCAGATGCTCAGC 5468
5365 TCACCGGTTGGGATGCTGTTAGATGCCATTAATGAGGAAGATTTGGGATGCCACC 5424
5469 TCACCGGTTGGGATGCTGTTAGATGCCATTAATGAGGAAGATTTGGGATGCCACC 5528
5425 GACAACGACAAAGGCTATCCGGCAATTTGTTTCAGCGACTGTTGGAATTTACGTTTCTC 5484
5529 GACAGCGACAAAGCTATCCGGCAATTTGTTTCAGCGACTGTTGGAATTTACGTTTCTC 5588
5485 CTTCATATCTAGTATTAAGCTTTTTCATGATGTTTATTAATGATGATGCTGCTCATTTCTC 5544
5589 CTCTCATACCTAGTATTAAGCTTTTTCATGATGTTTATTAATGATGATGCTGCTCATTTCTC 5648
5545 GAGAACTATAGCAGGCTACGAGGATGTACAGGAGGCTCTCACCGACGAGCATATGAT 5604
5649 GAGAACTATAGCAGGCTACGAGGATGTACAGGAGGCTCTCACCGACGAGCATATGAT 5708
5605 ATGCTACGAGATTTTGGCAACATTCGATCCGAGGCTACCCAGTACATACGATACGAC 5664
5709 ATGCTACGAGATTTTGGCAACATTCGATCCGAGGCTACCCAGTACATACGATACGAT 5768
5665 CAGCTGTCGAGTTCCTGGAGCTGCTGAGCGCGCTGAGATCCACAGCCCAAG 5724
5769 CAGCTGTCGAGTTCCTGGAGCTGCTGAGCGCGCTGAGATCCACAGCCCAAG 5828
5725 TACAAATCATATCATGAGGATGCTGCGGCGACATGATGCTGCTGCTGAT 5784
5829 TACAAATCATATCATGAGGATGCTGCGGCGACATGATGCTGCTGCTGAT 5888
5785 ATATTGATGCTGACCAAGGCTTCTTTCGCGCAAGGATTAATCCGATCGAGGAGACG 5844
5889 ATCTTCGAGCGCTTACGAAAGCTTCTTTCGCGCAAGGATTAATCCGATCGAGGAGACG 5948
5845 GGTCAATTTGCTGAGATGAGCGCGGACGAGGCTGATGATCCGCTGCTGTCG 5904
5949 GGTGAGATTTGCTGAGATGAGCGCGGACGAGGCTGATGATCCGCTGCTGTCATCA 6008
5905 ACATGTCGCGGCGGAGGATGCTGCGGCGGAGTACTGCGGCGGAGTACTGCGGCGG 5960
6009 ACATGTCGCGGCGGAGGATGCTGCGGCGGAGTACTGCGGCGGAGTACTGCGGCGG 6064

RESULT 10

ID US-08-808-793-26 STANDARD; DNA; UNC; 1237 BP.

AC xxxxxx

DT 01-JAN-1900

DE Sequence 26, Application US/08808793.

CC Sequence 26, Application US/08808793.

CC GENERAL INFORMATION:

CC APPLICANT: Soderlund, David M.

CC APPLICANT: Ingles, Patricia J.

CC TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS

CC TITLE OF INVENTION: AND USE THEREOF

CC NUMBER OF SEQUENCES: 32

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

CC STREET: Clinton Square, P.O. Box 1051

CC CITY: Rochester

CC STATE: New York

CC COUNTRY: USA

Tue Oct 14 14:18:10 1997

CC 12603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/808,793
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/034,361
CC FILING DATE: 24-DEC-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/012,649
CC FILING DATE: 01-MAR-1996
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Branan, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 26:
CC LENGTH: 1237 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC Sequence 1237 BP; 310 A; 309 C; 293 G; 325 T; 0 other;
Query Match 7.2%; Score 472; DB 70; Length 1237;
Best Local Similarity 76.6%; Pred. No. 0.00e+00;
Matches 679; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
Db 187 ACAACGTTCGCTGGCAATATTTCAAGTGTCTGACCTCAACACAGGAGTTCAGCCA 246
QY 4415 ACAGCTTTTGTGGAAATATTTTAAAGTGCAGGACATGAATGCAGAGCTCAGCCA 4474
Db 247 CGAATCATCCGACGCGAATCGTGCATCTTAGAGAACTACACCTGGGAGAACTCACC 306
QY 4475 CGAGATCATACCAATCGCAATCGCTCCGAGACGAGAACTACACGTGGTGAATTCAGC 4534
Db 307 GATGAACCTTTGACCATCTCGGCAAGCGGTATCTGCTGCTTCCAGTGGCCACCTTCAA 366
QY 4535 AATGAATTCGATCATGTAGTAAACGCTATCTGTCCTTTTCCAGTGGCCACCTTCAA 4594
Db 367 GGGATGATACAGATCATGACGACGCTATTTGATTCGAGAGAGTGGCCGCAACCTAT 426
QY 4595 AGGCTGGATCAATCAATGACGATGCTATCGATTACGAGAGGTGGACAAGCAACCAAT 4654
Db 427 ACAGGACGACCAATCATGATGATACCTGTACTTCTGCTGCTTCAATCATATTTGGCTCAT 486
QY 4655 TCGTGAAGCAACATCATATGATATTTATATTTCTGATTTCTTCAATATTTGGATTCCT 4714
Db 487 CTTCACCTCAACCTATTCATCGTGTGATCATGACGACAACTTTAAAGCAACAGAGAA 546
QY 4715 TTTACACTCAATCTGTTTCATGTTGTTTCATGATATTTTAAAGCAAGAGAA 4774
Db 547 AGCCGCGCGACCTTGGATGTTTCATGACTGAGGACCAAGAAATACATACATGCCAT 606
QY 4775 ACCAGGTGGATCATAGAAATGTTTCATGACAGAGATCAGAAAGTACTATATGCTAT 4834
Db 607 GAAGAAATGGTCTTAAAGAACTTTAAAGCTATCCGAGACCGAAGTGGCGGCACA 666
QY 4835 GAAAGAGATGGCTCTAAAGAACCTTTAAAGCAATTTCCAGACCAAGGTGGGACCA 4894
Db 667 AGCGATCGTGTTCGAGATGATGACGCAAGAAAGTTCGACATGATCATGTTGTCAT 726
QY 4895 AGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATATCATTTATTTATCAT 4954

Db 727 CGGCCTCAACATGTTGACGATGACGCTGATCCTACCAAGAGTTCGAGACCTTCAGCAC 786
QY 4955 TGGTCTGAACATGTTTCAACATGACCTCGATCGTATCGATCGCTCGGACAGTATACGC 5014
Db 787 TGTCTCGACTACCTCAACATGATATTCATCGTATATTCAGTTCAGAGTGCCTATTAAA 846
QY 5015 GGTCTTAGACTATATCAATGCGATATTCAGTATTTTTCAGTTCCGAATGCTCTATTAAA 5074
Db 847 AATGTTGCGCTTACGCTACCAATGCTTGTGAGCCATGGAACCTGTTCCGATTTGCTAGT 906
QY 5075 AATATTCGCTTTACGATATCACTATTTATGAGCCATGGAATTTATTTGATGATAGT 5134
Db 907 AGTCAATTTCTCAATTTAGTGTGATTTAGTATGATATATAGAAAAAATTTTGTGCTC 966
QY 5135 TGTCAATTTATCAATCTTAGTCTTGTACTTAGCGATATATTCGAGAAAGTACTTCGTGCTC 5194
Db 967 ACCACGTTTACTGAGGTTGTTGAGAGTACGGAAGTTCGCTGCTGCTGCTGCTGCTGCTG 1026
QY 5195 GCCGACCTGCTCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5254
Db 1027 GGTGCGAAGGTTATCGGACGTTATTTGCTGCGCTGCGCCACGCGC 1072
QY 5255 GGGAGCCAGGCAATTCGACACTGCTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5300

RESULT 11
US-08-682-433A-1 STANDARD; DNA; UNC; 6048 BP.

AC XXXXX
DT 01-JAN-1900
DE Sequence 1, Application US/08682433A.
CC Sequence 1, Application US/08682433A
CC GENERAL INFORMATION:
CC APPLICANT: Ken Stokes
CC APPLICANT: Jos e Morissette
CC TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
CC TITLE OF INVENTION: SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENET

IC TREATMENT OF SEQUENCES: 12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
CC STREET: One Liberty Place - 46th Floor
CC CITY: Philadelphia
CC STATE: PA
CC COUNTRY: U.S.A.
CC ZIP: 19103
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WordPerfect 6.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/682,433A
CC FILING DATE: Herewith
CC CLASSIFICATION: 514
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Paul K. Legaard
CC REGISTRATION NUMBER: 38,534
CC REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 568-3100
CC TELEFAX: (215) 568-3439
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6048 bases
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC Sequence 6048 BP; 1307 A; 1855 C; 1609 G; 1277 T; 0 other;

Query Match 4.9%; Score 320; DB 67; Length 6048;
Best Local Similarity 62.7%; Pred. No. 0.00e+00;
Matches 1162; Conservative 0; Mismatches 562; Indels 30; Gaps 18;

Tue Oct 14 14:18:10 1997

CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/334,029A
 CC FILING DATE: 02-NOV-1994
 CC CLASSIFICATION: 514
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Townsend, G. Kevin
 CC REGISTRATION NUMBER: 34,033
 CC REFERENCE/DOCKET NUMBER: 1459.0240000
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-371-2600
 CC TELEFAX: 202-371-2540
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3033 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: both
 CC TOPOLOGY: both
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1..3033
 CC Sequence 3033 BP; 860 A; 689 C; 687 G; 797 T; 0 other;

Query Match 4.8%; Score 312; DB 49; Length 3033;
 Best Local Similarity 62.3%; Pred. No. 0.00e+00;
 Matches 1210; Conservative 0; Mismatches 700; Indels 33; Gaps 21;
 Db 736 ATGATCCCTGCTCAGCAGTGGAGCTCTGGCTTTTGAAGATATCTATATGAAGAAAG 795
 Qy 3996 ATGATTTAATCAGTAGCTAGCTTTGGCATTAGAAGATGTACATCGCCACAAAGACC 4055
 Db 796 ACCATTAAGATATCCTGGAGTATGCTCAGACAGATATTCACCTACATCTTCATCTCGAA 855
 Qy 4056 ATACTCAGGATATTTATATCTATATGACAGAGATATTTAGCGTTATATCTTCTTGAA 4115
 Db 856 ATCTTCTAAATGGTGCATATGGGTATAAAGATATTTACATATATGCGTGGTGG 915
 Qy 4116 ATGTTAATCAGTGGTGGCGTCCGCTTCAAAGTGTACTTACCAACGCGTGGTGG 4175
 Db 916 CTGGACTTCTTAATGTTGATGCTCTAGTACTTTAGTAGCCCAACACTCTTGGGTAC 975
 Qy 4176 CTGGAATTCGTGATGTCTATGCTATCGCTTATCACTTCGTTGCTTCACTTGTGGAGCT 4235
 Db 976 TCAGACCTTGGCCCAATTAATCTCTACGGACACTGAGGGCCCTAAGACCCCTAAGAGCC 1035
 Qy 4236 GGTGGTATTCAGCCCTCAAGACTATGCGAAGCTTAAGAGCACTGAGACCACTACGTCC 4295
 Db 1036 TTGCTAGATTTGAAGAAATGAGGTAGTGGTCAACGCACTCATAGGAGCAATCCCTTCC 1095
 Qy 4296 ATGTCGGTATGCAAGGCATGAGGTGCTGTTAATGCGCTGGTACAACTATACCGTCC 4355
 Db 1096 ATGATGAACGTCTCTCGTGTGCTTATATCTGGCTAATATTTAGCATATGAGGATG 1155
 Qy 4356 ATCTCAATGCTGCTATGTTGGTGTCTAATATTTGGCTAATTTTGGCTAATTTTGGCTGTA 4415
 Db 1156 AATCTGTTTGTGCAAGTGTCTATGATGTGTCAACACCACTGATGGTCACGATTTCT 1215
 Qy 4416 CAGCTTTTGTGGAATAATTTAAGTGGAGGACATGA---ATGG---CACCAAGCTCA 4470
 Db 1216 ACATCTCAAGTGTCAACCGTCTCAGTGTGTTTGGCTGATGAACTGTAGTGAATGTG 1275
 Qy 4471 GC---CACGAGATCATACCAATCGCAATGCT---GC---GA-GAGCGAGAACT-ACACGTG 4522
 Db 1276 CGATGGAAGAACTGAAAGTAAACTTCGACAACTGGCTGGCTGGTGGTACCTGCTGCTT 1335
 Qy 4523 GG-TG---AATTCAGCAA-TGAATTTTCATCATGTAGTAAACGCGTATCTGTGCTTTTC 4577

Db 1336 CAAAGTTCACATTCACAGGCGTGGATGATATATATGATGACAGCAGTTGACTCTGTTAAT 1395
 Qy 4578 CAAAGTGGCCACCTTCAAAGCGTGGATACAAATCATGAACGATGCTATCGATTACAGGAG 4637
 Db 1396 GTAAATGAACAGCCGAAATACGAATACAGTCTCCTACATGTACATTTACTTTGTCATCTTC 1455
 Qy 4638 GTGGACAGCAACCAATTCGTGAACGAAACATCTACATGTATTTATATTTTCGTTATCTTC 4697
 Db 1456 ATCATCTCGGCTCATCTTCTCAGCTTGAACCTGTTCATTTGGTGTGTCATCATAGATAAATTC 1515
 Qy 4698 ATCATATTTGGATCCTTTTTCACACTCAATCTGTTTCATTTGGTGTGTTAATCATGATAATTT 4757
 Db 1516 AACCAACAGAA-AAAAAGCTTTGGAGTCA--AGATATCTTTTATGACAGAGACAGAG 1572
 Qy 4758 AATGACAAAGAAAGAAAGCAGTGGATGATCAATAGAAATGTTTCATGACAGAGATCAGAAA 4817
 Db 1573 AATATCTAATGCAATGAAGAGCTTGGCTCCAAAGAACCAACCAAAACCAATTCACAGG 1632
 Qy 4818 AAGTACTATAATGCTATGAAGAGATGGCTCTTAAGAACCATTAAGAGCCATTCACAGA 4877
 Db 1633 CCAGGGAACAAATTCCAAGGATGATATTTGACTTTAGTGACAAACCAAGCTTTTGTATATC 1692
 Qy 4878 CCAAGTGGCGACCAACAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATA 4937
 Db 1693 ACCATCATGTTCTTATATGCTCAACATGGTAACCATGATGTTAGAAAAAGAGGGGCAA 1752
 Qy 4938 ATCATTTATTTATTTGCTGTAACATGTTCCACCATGACCCCTCGATCGTGTACGATGG 4997
 Db 1753 ACTGAGTACATGGATATTTTACACTGGATCAACATGGTCTTTCATATTCCTGTTCACT 1812
 Qy 4998 TCGGACAGGTATACGGGCTCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGT 5057
 Db 1813 GGGAGATGTGTGTAAGCTAATCTCCTCAGACATTAACCTTACCTGTTGGTGGTGAAC 1872
 Qy 5058 TCCGAATCTCTATTAATAATATTCGCTTTACGATATCACTATTTTATGAGCCATGGAAT 5117
 Db 1873 ATTTTGTATTTTGTGGTGTAGTATCTCTCCATTTGTAGAAATGTTTCTCGCTGAGATGATA 1932
 Qy 5118 TTATTTGATGTAGTAGTGTGTCATTTTATCCATCTTAGGTCTGTGTTACTTAGCGATATATC 5177
 Db 1933 GAGAAGTATTTGCTGCTCCCTACCTGTTCCGAGTCACTCCGCTGGCCGAGATTGGAACA 1992
 Qy 5178 GAGAAGTACTTCTGCTGCCGCCACCTGCTCGAGTGGTGGTGGCGAAGTGGGCGT 5237
 Db 1993 ATCTACGCTCATCAAGAGGCGCAAGGGGATCGGCACTCTGCTCTTTGTTGATGATG 2052
 Qy 5238 GTCTTCGACTGGTGAAGGAGCCAAAGGSCATTCGGACACTGCTCTTCGCGTGGCCATG 5297
 Db 2053 TCCCTTCTCGCTGTTCACATCGGCTCTGCTTTTCTTCTGTTGTCATCTACGCTC 2112
 Qy 5298 TCGCTCGCGGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5357
 Db 2113 ATCTTTGGGATGTTCCAACTTTTGCCTACGTTAAAAAGAGGCTGGAATTAATGACATGTT 2172
 Qy 5358 ATTTTCGGGATGTCGTTCTTTCATGACGTGAAGAGAGAGAGCGCATTAAGACGCTCTAC 5417
 Db 2173 AACTTTGAGACTTTTGGCAACAGCATGATCTGCTTGTTCCTCAATCACCACCTCTCCCGCC 2232
 Qy 5418 AACTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTTTCAGATGTGACGTGACCCGCT 5477
 Db 2233 TGGAGGAGCTGCTGGCGCCCATCTCAACAGCGCACTTCCCGACTGTGACCCCTAAAAA 2292
 Qy 5478 TGGGATGGTGTACTGTGAGCGCATATCATATGAGAGCATGCGA-TCC-ACCCGACAGC- 5534
 Db 2293 GTTCACCCAGAGAGTTCAGTGAAGGGGACTGTGGGAACCCATCCGTTGGGGATTTTTAC 2352
 Qy 5535 GA-CAA--AGGCTATCGG-GCAATTG---TG-GTTACGCGA--CCGTTGGAATTAAGCTTT 5585
 Db 2353 TTTGTACCTACATCATCATATCTCTCTGCTGGTGGTGAACATGTACATCGCTGTCATC 2412
 Qy 5586 CTCTCTCATACATAGTATTAAGCTTTTGTATGATTTTAAATATGATGATGCTGCTCAT 5645
 Db 2413 CTGGAGAACTTTCAGCTGCGCCACCGCAAGAGAGAGCACTGAGCTCTGAGTGGAGGACGACTTT 2472

QY	5646	CTCGAGACTATAGTCAGGCCACCAGGAGACGTGCAAGAGGGTCTATCCGACGAGCAGTAC	5705
Db	2473	GAGATGTTCTTACGAGGCTTGGGAGAAAGTTCGACCTCTGACGCCACTCAGTTCATAGAGTTC	2532
QY	5706	GACATGTACTATGAGACTCTGGCAGCAATTCGATCCGGAGGCGCACCATACATACGCTAT	5765
Db	2533	TGCAAGCTCTCTGACTTTTCGACGTCGCTGGATCTCCCTCCCTCCTCATCGCAAGGCCAAAC	2592
QY	5766	GATCAGCTGTCCGAATTCCTGTGACGTACTTGGAGCCCCGGCTGCAGATCCACAAACCGAAC	5825
Db	2593	AAAGTCCAGCTCATATGCCATGGACCTGCCCATGGTGTAGTGAGGACCGGATCCCATGCGCTG	2652
QY	5826	AGTACAAGATCATATCATGATGACATACCATCTCTCGCGGTGACCTCATGTACTGCGCTC	5885
Db	2653	GACATCTTGTGCTTTTACAAA	2675
QY	5886	GACATCTCGACGCCCTTACGAA	5908

RESULT 13
ID US-08-511-828-1 STANDARD; DNA; UNC; 6344 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08511828.
CC Sequence 1, Application US/08511828
CC GENERAL INFORMATION:
CC APPLICANT: Herman, Ronald C
CC APPLICANT: Delgado, Stephen G
CC APPLICANT: Fish, Linda M
CC APPLICANT: Sangameswaran, Lakshmi
CC TITLE OF INVENTION: CLONED PERIPHERAL NERVE
CC TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT

CC NUMBER OF SEQUENCES: 8
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Syntex Corporation, Patent Department A2-200
 CC STREET: 3401 Hillview Avenue P.O. Box 10850
 CC CITY: Palo Alto
 CC STATE: CA
 CC COUNTRY: U.S.A.
 CC ZIP: 94303
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/511,828
 CC

Query Match	4.6%	Score 298;	DB 66;	Length 6344;
Best Local Similarity	63.9%;	Pred. 0.695e-291;		
Matches	891;	Conservative	0;	Mismatches 485;
				Indels 18; Gaps 13
Db	4070	AACTTCGACAAAGTCGCTATGGCTACCTCGCACTTCTTCAGGTGGCAACCTTCAAGGC	4129	
Qy	4539	AAATTGATCACTAGTAAACGGTATCTGTGCCTTTTCCAAAGTGGCCACCTTCAAGGC	4598	
Db	4130	TGGATGGACATAATGTATGACGCTGTGATTTCGGAGAGATCAACACGTACAGCCTAACTGG	4189	
Qy	4599	TGGATACAAATCATGAACGATCCTCATTCACGAGAGGTGGACAGCAACCAATTCGT	4658	
Db	4190	GAGAACAACTGTACATGTAACCTGTACTTCGTGCTTTTCATCATATTTTCGGTGGCTTTC	4249	
Qy	4659	GAAACGAACATCTACATCTATTAATTTTCGTATTTCTTCATCATATTTGGATCCTTTTC	4718	
Db	4250	ACGCTGAATCTCTTTGGGGTCAATAACGACAACTTCAACCAACAGAAAGAAAGCCTA	4309	
Qy	4719	ACACTCAATCTGTTCATTTGGTGTATCATATTGATTAATTTAATGAGCAAAAGAAAAGCA	4778	
Db	4310	GGAGGC-CAG--GACATCTTCATGACAGAAGCAGAGAAGTACTACAATGCCATGAAG	4366	
Qy	4779	GGTGGATATTAGAAATGTTTCATGACAGAGATCAGAAAAGTACTATAATGCTATGAA	4838	
Db	4367	AAGCTGGGCTCCAAAGAACCCAGAGCCCATCCACAGGGCCCTTGAATAGTACCAAGC	4426	
Qy	4839	AAGATGGGCTTAAAAAACCAATAAAGCCATTCCAAGCAAGGTGGCAGCACCAAGCA	4898	
Db	4427	TTCGTGTTTGACATCGTGACCAGCAAGCCTTTCACATCATCATCATGTTTCATCTGC	4486	
Qy	4899	ATAGTCTTTGAATATGATAACCGATAAGAAATTCGATTAATCATTTGTTATTCTTTGGT	4958	
Db	4487	CTCAACATGATCACCATGATGTGTGGAGACCGACGAGCGAGGAGAGAAGCAAGGTT	4546	
Qy	4959	CTGAACATGTTCAACATGACCCCTCGATCGTTACGATGCGTCGGACAGTATAACGCGGTC	5018	
Db	4547	CTGGGAGAAATCAACCAAGTCTTTTGGCGGTCTTCAGGGCGAGTGTGTGTGAAGATG	4606	
Qy	5019	CTAGACTATCTCAATCGCATATTCGTAGTATTTTCAGTTCGGAATCTCTATTAAAAATA	5078	
Db	4607	TTCCGCTTCGGACAGTACTTTCACCAAGGCTGGACGTTTCGACTTCATAGTGGTG	4666	
Qy	5079	TTCGCTTTAGGATATCAGTATTTAATGAGCCATGGAAATTTATTGTGATGATGATGTGTC	5138	
Db	4667	ATCCTGTCCATTTGGAGTCTGCTGTTTCTGCAATCCCTTAAAGTCACCTGGAACACTTC	4726	
Qy	5139	ATTTTATCCATCTTAGTCT--TGTACTTAGGATA-TTA--TCGA-GAAGTACTTCGTG	5192	
Db	4727	TCGCCAGCGCTCTTCGGGTCAATCGCTGCGCAGGATCGGCCGCATCCTCAGCGTATC	4786	
Qy	5193	TCGCCAGCCCTGCTCGAGTGGTGGTGTGGCGAAGTGGCGCGTCTCTTCAGTGGTG	5252	
Db	4787	CGAGCAGCAAGGGATTCGACGCTGCTCTTCGCCCTCATGATGTCCTTCGCCGCCCTC	4846	
Qy	5253	AAGGGAGCAAGGGCATTCGGACATGCTCTTCGCGTTTGGCCATGTCTGCTGCGCGCCGTG	5312	
Db	4847	TTCAACATCGGCTCTCTCTCTTCCTCGTCAATGTTTCATCTACTCCATCTTCGGCATGCC	4906	
Qy	5313	TTCAACATCTGCTCTGCTGTCTCTCTGCTCATGTTCATCTTTGGCATTTTCGGCATGTCG	5372	
Db	4907	AGCTTCGCTAACGCTGTGGACAGGCGCGGATCGACGACATGTTTCAACTTCAAGACCTTT	4966	
Qy	5373	TTCTTCATGCACTGAAGGAGAAGACGGCATTAACGACGCTCAACACTTCAAGACCTTT	5432	
Db	4967	GGCAACAGCATGCTGTGCCTGTTCCAGATCACCACCTCGGCCGCTGGGACGGCTCCTC	5026	
Qy	5433	GGCCAGAGCATGATCTGCTCTTTTCAGATGTGCGAGTTCAGCCGCTGGGATGTTGTA	5492	
Db	5027	AGCCCATCTCTAACACGGGGCTCCCTACTTCGACGCCCAACCTTGCACAGCAAGCGGC	5086	
Qy	5493	GAGCCCATTTCAAT--GAGGAAGC---A-TCCGATCC--ACCCGAC-ACGACAAAGGC	5543	
Db	5087	TCGCCGGGAACTTCGGGAGCCCGCGGTGGGCATCATCTTCTTTCACCACTCATCATC	5146	

QY	5544	TATCCGGGCAATGTGGTTCAGGACCGTGGAAFAACGTTTCTCCTCATACCTAGTT	5603
Db	5147	ATCTCTTCCTCATCGTGTGTCACATGATACATCGGAGTGTCTGGAGAACTTCAACGTG	5206
QY	5604	ATAGCTTTTGTAGTATTAATATGATATGTGTCTATCTCGAGAACTATAGTCAG	5663
Db	5207	GCACCCAGGAGACGAGCGGAGCCCTGACGAGGAGCGACTTCGACATGTTCTATGAGACC	5266
QY	5664	GCCACGAGACGTGGAAGAGGCTCTAACCGACGACGACTACGACATGACTATGAGATC	5723
Db	5267	TGGGAGAAGTTTCAGCCGGAGGCCACCCAGTTCATGTCCTTTCTGCCCTCTCAGACTTC	5326
QY	5724	TGGCAGCAATTCGATCGGAGGCGACCCAGTACATACGCTATGATCAGCTGCGGAATTC	5793
Db	5327	CGGACAGGCTCTCCGGCCCTCTTAGAATCCCAACCCAGCAAGATATATTAATCCAG	5386
QY	5784	CTGGACGCTACTGGAGGCCCGCGCTGACATCCATGCTGCTGACATCTCTGACATCATCG	5843
Db	5387	ATGGACCTGCGGTTGGTCCCGGGGATGAAGATCCATCGTGTGACATCCTTTTGGCTTC	5446
QY	5844	ATGGACATACCATCTGTCGCGGTGACCTCATGCTGCTGACATCTCTGACATCTCTGACG	5903
Db	5447	ACAAAGACGCTTT 5460	
QY	5904	ACGAAAGACTTCTT 5917	

RESULT 14
 ID US-08-775-475-1 STANDARD; DNA; UNC; 6524 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application US/08775475.
 CC Sequence 1, Application US/08775475
 CC GENERAL INFORMATION:
 CC APPLICANT: Wood, John N.
 CC APPLICANT: Akopian, Armen N.
 CC TITLE OF INVENTION: Ion Channel
 CC NUMBER OF SEQUENCES: 31
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: ZENPECA Pharmaceuticals
 CC STREET: 1800 Concord Pike, P.O. Box 15437
 CC CITY: Wilmington
 CC STATE: Delaware
 CC COUNTRY: USA
 CC ZIP: 19850
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/775,475
 CC FILING DATE:
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Hohenschutz, Liza D.
 CC REGISTRATION NUMBER: 33,712
 CC REFERENCE/DOCKET NUMBER: PHM.70086
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (302) 886-7466
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 6524 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: CDNA
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 204..6077
 CC Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T; 0 other;
 SO

QY 5544 TATCGGCAATTTGGTTCAGCGACCGTGGGAATAAGTTTCTCCCTCATACCTAGTT 5603
DB 5331 ATCTCCTTCTCATCGTGGTCAACATGATACATCGAGTATCTGGAGAACTTCAACGTA 5390
QY 5604 ATAAGCTTTTGTAGTATTAATATATACATCTGCTGCTATCTCGAGAACTATAGTCAG 5663
DB 5391 GCCACGAGGAGAGCAGGAGCCCTCGAGGAGGACGACTTCGACATGTTCTATGAGACC 5450
QY 5664 GCCACGAGGAGGAGGAGGAGGCTTACCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5723
DB 5451 TGGGAGAGTTCGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5510
QY 5724 TGGCAGCAATTCGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5783
DB 5511 GCGGACAGGCTCTCGGCGCTCTTAGATCCCAACCCACACGAGATATATATCCAG 5570
QY 5784 CTGGAGCTACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5843
DB 5571 ATGACCTGCGGTTGGTCCCGGGGATAGATCCCAACCCACACGAGATATATATCCAG 5630
QY 5844 ATGACATACCATCTGTGCGGTTGACCTCATGCTACTGCTGCTGCTGCTGCTGCTGCT 5903
DB 5631 ACAAGAACGCTTT 5644
QY 5904 ACGAAGACTTCTT 5917

RESULT 15
ID US-08-669-656A-1 STANDARD; DNA; UNC; 6524 BP.

AC xxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08669656A.
CC Sequence 1, Application US/08669656A
CC GENERAL INFORMATION:
CC APPLICANT: Wood, John N.
CC APPLICANT: Akopian, Armen N.
CC TITLE OF INVENTION: Ion Channel
CC NUMBER OF SEQUENCES: 31
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: ZENECA Pharmaceuticals
CC STREET: 1800 Concord Pike, P.O. Box 15437
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: USA
CC ZIP: 19850
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/669,656A
CC FILING DATE: 24-JUN-1996
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hohenschutz, Liza D.
CC REGISTRATION NUMBER: 33,712
CC REFERENCE/DOCKET NUMBER: PHM.70086
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 886-7466
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6524 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 204..6077
SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T; 0 other;

Query Match 4.5%; Score 296; DB 67; Length 6524;
Best Local Similarity 63.8%; Pred. No. 1.31e-288;
Matches 890; Conservative 0; Mismatches 486; Indels 18; Gaps 11;
DB 4254 AACTTCGACAACTGCTATGCGCTACCTCGCACCTTCTTCAGGTGGCAACCTTCAAAGGC 4313
QY 4539 AATTTTCGATCATGTAGTAACGGGTATCTGTGCTTTTTCGAAGTGGCCACCTTCAAAGGC 4598
DB 4314 TGGATGACATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4373
QY 4599 TGGATGACATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4558
DB 4374 GAGAACAACCTTGTACATGTACCTGTACTTCTGCTGTTTTCATCATTTTCGTTGGCTTCTTC 4433
QY 4659 GAAAGCAACATCTACATGTATTTATTTCTGTTTCTTCATCATTTTGGATCCTTTTTC 4718
DB 4434 ACGTGTATCTTTTGTGGGTCATTAATCGACAACCTTCAACCAACAGAAAAAAGCTA 4493
QY 4719 ACATCTCAATCTGTTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4778
DB 4494 GGAGGC-CAG--GACATCTTTCATGACAGAGAGCAGAGAGTACTACATGTCATGAAG 4550
QY 4779 GTGGATCATTAGAAATGTTTCATGACAGAGATCAGAAAAAGTACTATAATGCTATGAAA 4838
DB 4551 AAGCTGGGCTCCAGAAACCCAGAGCCCATCCAGCGCCCTGTAATAAGTACCAAGGC 4610
QY 4839 AAGATGGGCTTAAAGAACCATTTAAAGCCATTTCCAGACCAAGGTGGCGCACCAAGCA 4898
DB 4611 TTGCTGTTTTCATGTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 4670
QY 4899 ATAGTCTTTGAAATAGTAACCGGATTAAGAAATTCGATATAATCATTTATTTATTTATTT 4958
DB 4671 CTCACATGATGATCACCATGATGTTGGAGACGACGACGACGACGACGACGACGACGACG 4730
QY 4959 CTGAACATGTTTACCATGACCTCGATCGTTACGATCGCTCGGACGATTAACCGCGGTC 5018
DB 4731 CTGGCAGAAATCAACAGTTCTTTTGGCGCTCTTTCACGCGCGAGTGTGTGATGAAGATG 4790
QY 5019 CTAGACTATCTCAATGGATATTCGTAGTTATTTTTCAGTTCCGAATGCTCTATTTAAAAATA 5078
DB 4791 TTGCGCTCGGACAGTACTACTTTCACCAACGGCTGGAGACGTTTCGACTTCATAGTGGTG 4850
QY 5079 TTGCGTTTACGATATCACTATTTTATGAGCCATGGAATTTATTTATGATGATGATGATG 5138
DB 4851 ATCTGTCATTTGGGAGTCTGCTGTTTCTGCAATCTTAAAGTACGTTGAAATCTACTTTC 4910
QY 5139 ATTTTATCTATCTAGTCT--TGTACTTAGCGATA-TTA--TCGA-GAAGTACTTCTGTG 5192
DB 4911 TCCCGGACGCTCTTCCGGGTCTATCCGCTCGGACGAGTCCGCGCATCTCTCAGGCTGATC 4970
QY 5193 TCGCGGACCTGCTCCGAGTGGTGGCGAGTGGCGAAAGTGGCGGTGCTCTCGACTGGTG 5252
DB 4971 CGAGCAGCAAGGGGATTCGACGCTGCTCTTGGCCCTCATGATGTCCTGCGCGCCCTC 5030
QY 5253 AAGGAGCCCAAGGGCATTCGACACACTCTCTGCGGTGGCCATGTCGCTGCGCGCCCTG 5312
DB 5031 TTCAACATCGGCT 5090
QY 5313 TTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5372
DB 5091 AGCTTCGCTAACGTCGTGGAGCGGCGCATCGACGACATGTTTCAACTTCAAGACCTTT 5150
QY 5373 TTCTTTCATGACGCTGAAGGAGAGAGGCGCATTAACGACGCTTACAACTTCAAGACCTTT 5432
DB 5151 GGCAGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5210
QY 5433 GGCAGAGCATGATCT 5492
DB 5211 AGCCCATCTCTCAACGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5270
QY 5493 GACCCCATTTATCAAT--GAGGAGC---A-TGGATCT--ACCGAC-ACGAGCAAGGC 5543
DB 5271 TCCGGGGGAACTGCGGGAGCCCGGCGGTCATCTTCTTCCACCATCATCATC 5330

Tue Oct 14 14:18:10 1997

QY 5544 TATCCGGGCAATTGGTTCACGACCGTGGAAATACGTTTCCTCTCATACCTAGTT 5603
Db 5331 ATCTCCTTCTCATCGTGGTCAACATGATACATCGCAGTGAATCTCGGAGAACTTCAACGTA 5390
QY 5604 ATAAGCTTTTGTATAGTTTAAATATGTACATGCTGTCATCTCGAGAACTATAGTCAG 5663
Db 5391 GCCACCGAGGAGACGACGAGCCCTGAGCGAGGACGACTTCGACATGTTCTATGAGACC 5450
QY 5664 GCCACCGAGGAGACGTCANAGAGGTCCTAACCGACGACGACTACGACATGCTATGAGATC 5723
Db 5451 TGGGAGAAAGTTTCGACCGGAGGCCACCCAGTTCATTCCTTTTTCGCCCTCTCAGACTTC 5510
QY 5724 TGGCAGCAATTCGATCCGGAGGACCCAGTACATACGCTATGATCAGCTGTCCGAATTC 5783
Db 5511 GCGGACACGCTCTCCGGCCCTCTTAGAATCCCAACCCAGCAAGAAATATATATATCCAG 5570
QY 5784 CTGGACGTACTGGAGCCCCCGCTGACAGATCCCAACCCAGCAAGTACAGATCATATCG 5843
Db 5571 ATGGACCTGCGGTTGGTCCCGGGGATAGATCCACTGTCTGGACATCCTTTTTCGCTTC 5630
QY 5844 ATGGACATACCATCTCTGCGGCTGACCTCATGTACTGGGTCGACATCCTCGACGCCCTT 5903
Db 5631 ACAAGAAGCTCTT 5644
QY 5904 ACGAAGACTTCTT 5917

Search completed: Sat Oct 11 06:36:48 1997
Job time : 4319 secs.

WIREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Oct 11 03:17:51 1997; MasPar time 670.28 Seconds
Tabular output not generated. 956.065 Million cell updates/sec

Title: >US-08-554-424-7
Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTACACGTTGGCGCATAG.....ACGGAGTATTAGCTCTAGA 6513
Comp: AGATCTGAACGGCGTATC.....TGGCTCATATCGAGATCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 134151 seqs, 49196315 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq27
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 10.670; Variance 6.369; scale 1.675

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	6513	100.0	6513	22	T18986 Drosophila para volta	0.00e+00
2	6513	100.0	6513	22	T33238 Drosophila para volta	0.00e+00
3	352	5.4	7555	13	Q81328 Cardiac sodium channel	4.82e-219
4	344	5.3	7555	1	Q05831 Cardiac sodium channel	2.17e-213
5	312	4.8	3033	22	T30192 Peripheral nervous sy	8.04e-191
6	312	4.8	6452	22	T30193 Peripheral nervous sy	8.04e-191
7	308	4.7	6371	22	T30194 Peripheral nervous sy	5.26e-188
8	308	4.7	6404	22	T30195 Peripheral nervous sy	5.26e-188
9	177	2.7	2308	12	Q71202 scd131, a subclone of	9.75e-97
10	96	1.5	2416	12	Q71200 scd61, a subclone of	2.91e-42
11	93	1.4	1047	2	Q10572 Human Natriuretic pep	2.60e-40
12	85	1.3	1047	2	Q10572 Human Natriuretic pep	8.70e-36
13	50	0.8	204	1	N81164 Base substituted E.co	1.59e-13
14	44	0.7	91	9	Q51746 Oligonucleotide probe	4.41e-10
15	45	0.7	91	9	Q51746 Oligonucleotide probe	1.20e-10
16	48	0.7	204	1	N81164 Base substituted E.co	2.30e-12

17	43	0.7	6725	15	Q87834	Human neuronal calciu	1.61e-09
18	38	0.6	114	12	Q70465	Generic DNA sequence	9.03e-07
19	37	0.6	114	12	Q70469	Generic DNA sequence	3.10e-06
20	36	0.6	114	12	Q70468	Generic DNA sequence	1.05e-05
21	36	0.6	114	12	Q70467	Generic DNA sequence	1.05e-05
22	39	0.6	114	12	Q70469	Generic DNA sequence	2.60e-07
23	38	0.6	114	12	Q70467	Generic DNA sequence	9.03e-07
24	38	0.6	114	12	Q70465	Generic DNA sequence	9.03e-07
25	38	0.6	114	12	Q70468	Generic DNA sequence	9.03e-07
26	38	0.6	114	12	Q70466	Generic DNA sequence	9.03e-07
27	36	0.6	114	12	Q70470	Generic DNA sequence	1.05e-05
28	42	0.6	811	5	Q29261	Human calcium channel	5.82e-09
29	39	0.6	1028	4	Q27091	XY26 probe.	1.05e-05
30	39	0.6	1089	4	N92576	Sequence of the 1.lkd	2.60e-07
31	36	0.6	1809	19	T15008	Mouse Elf-1 cDNA.	1.05e-05
32	41	0.6	2050	5	Q29265	Human calcium channel	2.08e-08
33	36	0.6	3109	4	Q24982	DNA induced in human	1.05e-05
34	37	0.6	3765	5	Q31890	FMR-1 gene for detect	3.10e-06
35	39	0.6	5904	6	Q37813	Sequence encoding the	2.60e-07
36	37	0.6	5975	1	N91778	Rabbit skeletal muscle	3.10e-06
37	37	0.6	5975	14	Q87978	Rabbit skeletal calci	3.10e-06
38	39	0.6	6575	15	Q84655	Human neuronal calciu	2.60e-07
39	35	0.5	75	13	Q79643	Longest observed alle	3.54e-05
40	35	0.5	954	1	N90505	DNA encoding Group B	3.54e-05
41	35	0.5	1433	24	Q99243	Insulin like growth f	3.54e-05
42	35	0.5	1438	1	Q04550	EcoRI-EcoRI fragment	3.54e-05
43	35	0.5	2374	13	Q79630	Partial FRAXE region	3.54e-05
44	35	0.5	6407	23	T36035	rchd528 gene differen	3.54e-05
45	35	0.5	7860	23	T44380	Stretch-activated cat	3.54e-05

ALIGNMENTS

RESULT 1
ID T18986 standard; cDNA; 6513 BP.
AC T18986;
DT 15-OCT-1996 (first entry)
DE Drosophila para voltage-activated sodium channel cDNA.
KW Para voltage-activated sodium channel; cation channel; t1pE;
KW antisense; ss
OS Drosophila melanogaster.
PN WO9615220-A1.
PD 23-MAY-1996.
PF 06-NOV-1995; U14378.
PR 10-NOV-1994; US-337339.
PA (MERI) MERCK & CO INC.
PA (UUNY) UNIV NEW YORK STATE.
PI Arena JP, Feng G, Hall LM, Liu K, Van Der Ploeg LHT;
PI Wang P, Warnke JW;
DR WPI; 96-259828/26.
PT Co-expression of voltage-activated cation channel alpha and beta sub-units - esp. para and tip E sub-units of drosophila voltage activated sodium channel protein in biologically active form
PS Claim 19; Page 36-40; 52pp; English.
CC A full-length cDNA clone (T18986) codes for the Drosophila para voltage-activated sodium channel (VASC), a protein responsible for the fast depolarising phase of the action potential that underlies electrical signaling in neurons, muscles, etc. Functional expression of the para VASC requires the co-expression of the para alpha subunit with t1pE, a putative Drosophila VASC beta subunit. The para VASC cDNA clone was obt'd. from 3 overlapping regions of para cDNA isolated by PCR amplification using primers (see also T18987-92) based on a published para sequence. Recombinant host cells (E.coli, yeast or mammalian or insect) expressing the Drosophila para VASC can be used to isolate para VASC in biologically active form. Antisense constructs can block expression of the gene.
SQ Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T;
Query Match 100.0%; Score 6513; DB 22; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 tctagacgttgccgcacatagacaagagatccgactctctatctgaggagaac 60

Tue Oct 14 14:18:08 1997

QY	1	TCATAGAGTTGGCGCATACACAAATGACAGAAAGATTCGACATCGATATCTGAGGAAGAC	60
Db	61	gcagttgttcctcccttaccacccggaatcatttggtgcaaatcgaaacacgaacgctg	120
QY	61	GCAGTTTGTTCCTGCTTATCCCGGATCATTTGGTGCNAATCGAACAACGATTCGGC	120
Db	121	ctgaacatgaagcagaagagctggaaagaaagagacagagagaggtgcccgcgat	180
QY	121	CTGAACATGAAGCAGAAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCGCGAT	180
Db	181	atggtgcgaagaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac	240
QY	181	ATGGTGCGCAAGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA	240
Db	241	cacaacccgattctacacttgaaacaggggtgccaatacctgttcgaatgcagggcagct	300
QY	241	CACAACCCGATCTACACTTGAACAGGGGTGCGCAATACCTGTTCGATTCGACGGCAGCT	300
Db	301	tcccgcgggaattgctccactctctcagggatctcgatccctactacagcaatgtac	360
QY	301	TCCCGCGGAATTGCGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360
Db	361	tgacattcgtagttgaagcaagaaagatatatttttcgtcttttcgcatcaaaagcaa	420
QY	361	TGACATTCTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCGATTCATCAAAAGCAA	420
Db	421	tgtgagatgcacattcaatccgacacgctcgtgtggccatttacattctagtcac	480
QY	421	TGTGGATGCTCGATCAATCAATCCGATACGTCGTCGTGCCATTTACATTTCTAGTGCATC	480
Db	481	cattatttccttattcatcaacaaattcgtcaaatcgtcaaatcgtcaaatcgtcaaat	540
QY	481	CATTATTTTCCCTATTATCATCATCACCAAAATTCGTCGAATGCAATCGATATATGC	540
Db	541	cgacaacgcccaggttgagtcacagtgagtgatattcccggaatctacacattgaa	600
QY	541	CGACAACGCCCCAGGTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTGAA	600
Db	601	cagctgttaagtgatggcagaggtttcattttatgcgcgtttacgtatcttagatg	660
QY	601	CAGCTGTTAAGTGATGGCAGAGGTTTCAATTTATGCGCGTTTACGTATCTTAGAGATG	660
Db	661	catggaattggctgagctcgtagtaagtagcttagcttagcttagcttagcttagct	720
QY	661	CATGGAAATGGCTGGATTCGTAGTATATAGCTTTAGCTTATGTGACCATGGGTATAGAT	720
Db	721	taggtaactagcagccctgcgaacgttttaggggtgctgagagcgttaaaacgtagcca	780
QY	721	TAGGTAATCTAGCAGCCCTGGAACGTTTAGGGTGTGCGAGGCGCTTAAACCGTAGCCA	780
Db	781	ttgtccaggttgagacacatcgtgcgcgcgtcatcgaatcgggtgaagaatctgcgcg	840
QY	781	TTGTCCAGGCTGGAAGACCATCGTCGGCGCGTCATCGAATCGGTGAAGAACTGCGCG	840
Db	841	atgtattatctgaccatgttctccctgtcgggtgttcggtgagctgagctcagaatct	900
QY	841	ATGTGATATCTGACCATGTTCTCCCTGCTGGTGTTCGGCTTATGGGCTTACAGATCT	900
Db	901	atatggcgctgcacccagagagtgatcaagaagttcccgctggacggttccctggggca	960
QY	901	ATATGGCGTGTACCCGAGAGTGCATCAAGAGTTCCTCCGCTGGACGGTTCTCTGGGCA	960
Db	961	atctgaccagagagactgactacaaatcgcaatagctccaattggtattccaggg	1020
QY	961	ATCTGACGAGAGACTGGGACTATCAAAATCGAAATAGTCCAAATTTGGTATTCCGAGG	1020
Db	1021	acaggggcatctatttcgttatcggaatatatccggtgctgggggaatgcgacgacg	1080
QY	1021	ACGAGGCAATCTCATTTCCGTTATGCGCAATATATCCGTCGGGGCAATGCGACGACG	1080
Db	1081	attacgtgtcctgcaggggtttgttcggaatccgaattatggttacaccagcttcgatt	1140
QY	1081	ATTACGTTGCTGCAGGGTTTGTTCGGAATCCGAATTCATGACAAATCTCTTTTATCGAGCCCTCGACAC	1140
Db	1141	cgttoggatgggcttctcgtccgctccgctcgtgatgacacaggaacttctggagatc	1200
QY	1141	CGTTCCGATGGGCTTCTCTGTCGCGCTTCCCGCTTGATGACACAGGACTTCTGGGAGATC	1200
Db	1201	tgtaccagctggtgttgccgcccgcgacacatggacatgctgtttttatagatca	1260
QY	1201	TGTACCAGCTGTTGTCGCGCGCGGACCATGGACATGCTGTCTTTTATAGTATCA	1260
Db	1261	tcttctagtttcttctctcttcttcttcttcttcttcttcttcttcttcttcttctt	1320
QY	1261	TCTTCTAGTTTCTATCTATCTGTGAATTTGATTTTGCCCTTGTTCGCATGCTGATG	1320
Db	1321	acgaattgcaagagagcgcgaagaagaagagcgtgcgaagaagagagagagagag	1380
QY	1321	ACGAATTTGCAAGAGAGCGCGCAAGAGAGGCTGCCGAAGAGAGGCGATACGTGAAG	1380
Db	1381	cgggaagctgcccgcgcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaag	1440
QY	1381	CGGAAGAAGCTGCCGCGCAAGAGCGCAAGCTGGAGAGCGGGCAATGCGGAGGCTC	1440
Db	1441	aggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	1500
QY	1441	AGGCAGCAGCGGATGCGGCTGCCGCGAAGAGGCTGCATGCTATCGGAATGCGCAAGA	1500
Db	1501	gtccgagctattcttgcacatgctgagctgagctgagctgagctgagctgagctgag	1560
QY	1501	GTCCGACGCTATTCTTGTATCATGCTATGAGCTATTTGTGTGGCGGAGAGGGCAACGATG	1560
Db	1561	acaacaacaagaagaagatgctcattcggagcgtcgaggtggaggtggaggtggag	1620
QY	1561	ACAACAACAAGAGAGATGTCATTCGGAGCTCGAGGTGGAGTCTGGTCTGGTGGAGCG	1620
Db	1621	ttatacaagaacacacagcactaccacacacacacacacacacacacacacacac	1680
QY	1621	TTATACAAAGACAACAGCAGCAGCTTACCACAGCACACACAGCTTACCANAAGTTCTGTAAGTGA	1680
Db	1681	gcagcactcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct	1740
QY	1681	GCAGCAGCTCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1740
Db	1741	ctcacaagctacacgacgagcagcagcagcagcagcagcagcagcagcagcagcag	1800
QY	1741	CTCACAAGTACAGATACGGAACGAGCTGGCGCTTTGGTATACCCCGTACGATCGTA	1800
Db	1801	agccattggtattgtaacatcatcaggaatgccagcagcagcagcagcagcagcag	1860
QY	1801	AGCCATTGGTATTGTCAACATATCAGATATGCCAGCAGCTTGCCTATGCGGAGACT	1860
Db	1861	cgaatgcttcaccccgatgctcgaagaagaatggggccatcagtcgctgtactatg	1920
QY	1861	CGAATGCGGTCAACCGGATGTCGGAAGAAATGGGGCCATCATAGTCCCGTGTACTATG	1920
Db	1921	gcaatctaggtccac	1980
QY	1921	GCAATCTAGGTCCCGACACTCATCTATACCTTCGATACCTTCCCGAATATGATACCT	1980
Db	1981	cacatggcgatctactcggcgagcagcagcagcagcagcagcagcagcagcagcag	2040
QY	1981	CACATGGCGATCTACTCGGGGATGCGCGCTATGGGGGTCAGCAACATGACCAAGAGA	2040
Db	2041	gcaaatgcaac	2100
QY	2041	GCAAAATGGCAACCGCAACACACAGCAATCAATCAGTGGGGCGGCAACCAATGGCGGCA	2100
Db	2101	cctgtctgac	2160
QY	2101	CCTGTCTGACACCAATCACAGCTCGATATCGGACTACGAAATTTGGCTGGAGTGCA	2160
Db	2161	cggagagcagctggcagattacacacacacacacacacacacacacacacacac	2220
QY	2161	CGGACGAAGCTGGCAAGATTAAACATCATGACAAATCTCTTTTATCGAGCCCTCGACAC	2220

QY 4381 TAATATTGGCTAAATTTTGGCCATAATGAGGTGTACAGCTTTTGCTGAAAATATTTTA 4440
DB 4441 agtcgaggaacatgaattggcacgaagctcagccagccagagatcataccaaatcycaatgcct 4500
QY 4442 AGTCGGAGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCATAATGCCAATGCCT 4500
DB 4501 gcgagcgagaactaacacgtgggtgaattcaccaatgaatttgcgatcatgtagttaacg 4560
QY 4502 GCGAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG 4560
DB 4561 cgtactctgctttccaagtggccacctccaaggcttgatacacaatatcatgaagatg 4620
QY 4562 CGTATCTGTGCTTTTCCAAGTGGCCACTTCAAAGGCTGGATACAAATCATGAACGATG 4620
DB 4621 ctatcgattcacgagaggtggacaagcaaccaattcgtgaacgaacatctacatgtatt 4680
QY 4622 CTATCGAATTCACGAGAGTGGACAAGCAACCAATTCGTGAACGAACATCTACATGTATT 4680
DB 4681 tatattcgtattcttcattcatatttggatcccttttccacactcaatttgttcatgttg 4740
QY 4682 TATATTTCTGTATCTTCATCATATTTGGATCTCTTTTTCACACTCAATCTGTTCATTGGTG 4740
DB 4741 ttatcattgataaatttaataagcaaaaagaaaaagcagggtgagcattagaagaattgtca 4800
QY 4742 TTATCATTTGATATTTTATGATGCAAAAGAAAAAGAACGAGTGGATCATTAAGAAATGTCA 4800
DB 4801 tgacagaagatcagaanaagtagcta taatgctatgaataaatgggtctcaaaaaaccat 4860
QY 4802 TGACAGANGATCAGAAAAGTAGTATAATGCTATGAAAAGATGGGCTCTAAAACACCAT 4860
DB 4861 taaagccattccaagcacaaggtggcgaccacaagaatagctcttgaaataglaacgg 4920
QY 4862 TAAAGCCATTCCAAGACCAAGTGGCGACCAACCAATATGCTTTGAAATAGTAACGG 4920
DB 4921 ataagaattcgataataatcatatttatctattcgttgctgaacatgttcaaccatgccc 4980
QY 4922 ATAGAATAATTCGATTAATCATTAATGTTATGTTATGTTGTTGCTGAACATGTTACCATGACC 4980
DB 4981 tcgatcgttacgatgcgtcggaacgcgtataacgcggtcctagactatcctaatgggat 5040
QY 4982 TCGATCGTTAGCATGCGTCGAGCACGATTAACGGGTCCTAGACTATCTCAATGCGATAT 5040
DB 5041 tcgtatgtatttcagttccgaatgtctattaaaaattcgtttacagatatcaactatt 5100
QY 5042 TCGTAGTTATTTTTCAGTTCCGAATGCTATTAATAAATATTCGTTTTACGATATCATATT 5100
DB 5101 ttattgagccatggaattatttgatgtagttgctcattttatccattttaggtcttg 5160
QY 5102 TTATTGAGCCATGGAATTTATTTGATGTAGTGTGTTTCATTTTATCCATTAGGTCCTG 5160
DB 5161 tactlagcatattatcagaaagtactcgtgctgcgcgacctcctccgagtggtgcgtg 5220
QY 5162 TACTTAGCGATATATTCAGAAAGTACTTCGTGTCGCCGACCCTCTCCGAGTGTGCGTG 5220
DB 5221 tggcgaagtggccggtgcttccttcagctgggtgaaggagcgaaggcattccggacactgc 5280
QY 5222 TGGCGAAAGTGGGCGGTGCTTCGACTGCTGTAAGGGAGGCCAAGGCCATTCGGACATGC 5280
DB 5281 tcttcgctggcgaatgctgcgtgcgcgcgcctgttcaacatctgcctgctgtcttcttg 5340
QY 5282 TCITCGGCTWGGCATGTGCTGCGGCCCTGTTCAACATCTGCTGCTGTGTTCTCTFG 5340
DB 5341 tcatgttcatcttttgcatttttggcatgtcttcttcacgtcacgtgaagagaagagcg 5400
QY 5342 TCATGTTATCTTTGGCCATTTTCGGCATGTCGTTCTTATGACGTGAAGGAGAGAGCG 5400
DB 5401 gcattaacagcgtctacaacttcaaaccctttggccagagcatgatcctcgtctcttcaga 5460
QY 5402 GCATTAACGAGCTTACAACTTCAAGACCTTTGGCCAGACGATGATCCTTCCTTTCAGA 5460
DB 5461 tgtcagcgtcagcgggttggatgggttactggaacccattatcaatgaggagcatgcg 5520

RESULT 2
ID T33238 standard; cdna; 6513 BP.

Db 3841 aatccagcgtgattgctgcccgcttccgactataaagaaatttccgactcttagccgctg 3900
Qy 3841 AATATCCAGCTGATGCTGCCCGATTGCTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
Db 3901 acgatgactcgcggtctctggaagagatggggcaatttccgactgaaaccttttcaattaa 3960
Qy 3901 ACGATGACTCGCCGCTCTGGCAAGATGGGCAATTTACGACTGAAACTTTTCAATTAA 3960
Db 3961 ttgaataataattttgaacagctgttatacactatgattttaaagtagcttagctt 4020
Qy 3961 TTGAAAAATAATATTTTGAACAGCTGTATACACTATGATTTAATAGTAGTACTAGCTT 4020
Db 4021 tggcattagaagatgacatctgcacaaagaccatactcagagataattttatactata 4080
Qy 4021 TGGCATTAGAGATGTACATCTGCCACAAAGACCATACTGCAGGATATTTATACTATA 4080
Db 4081 tggacagaatatttcggtttattctctctcttggaaatgttaatacagtggttggcgctg 4140
Qy 4081 TGGACAGAAATATTTACGGTTATATTTCTTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
Db 4141 gcttcaaaagttaacttaccacacgctgggttctgctcgatttctgattgctcagtgat 4200
Qy 4141 GCTTCAAAAGTACTTACCAACGCGTGGTGTGGCTCGATTCGATTCGTATGCTATGTTAT 4200
Db 4201 cgtcttcaactctgtcttcaacttgttgagctgggtgtattcaagccttcaagacta 4260
Qy 4201 CGCTTATCAACTCTGCTTCACTTGTGGAGCTGGTGTATTCAAAGCCTTCAAGACTA 4260
Db 4261 tgcgaacgttaagacactgagacacactacgtgcgatgcccgtatgcagggcatgaagg 4320
Qy 4261 TGCGAACGTTAAGACACTGAGACACACTACGTCGCTATGCCGTATGCAGGGCATGAGGG 4320
Db 4321 tgcgtcttaagtgcgtgttacaagctaaccgtccatcttcaatgtctattggtgtgtc 4380
Qy 4321 TCGTCTGTTAATGCGCTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATGGTGTCT 4380
Db 4381 taatatttggctaattttggcataaagggtgtacagcttttctgctggaataatttta 4440
Qy 4381 TAAATATTTGGCTAATTTTGCATAATATGGGTGTACAGCTTTTGTCTGGAAATATTTTA 4440
Db 4441 agtcgaagacatgaatggcagaagctcagccagagatcataccaatacgaatgctt 4500
Qy 4441 AGTCGAGAGACATGAATGGCAGAAAGCTCAGCCAGAGATCATCAAAATCGCAATGCTT 4500
Db 4501 gcgagagcagactacacgtgggtgaattcagcaatgaattcgcattcatgtagtaacg 4560
Qy 4501 GCGAGCGGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGTACG 4560
Db 4561 cgtatctgtgcttttccaagtggccaccttcaaggctggatacaaatcatgaacgatg 4620
Qy 4561 CGTATCTGTGCCCTTTTCCAAGTGGCCACCCTTCAAAGCTGGATACAAATCATGAACGATG 4620
Db 4621 ctatcgattcaagaggttggcaagaacacaaatcgtgaaacgaacatctcatgtatt 4680
Qy 4621 CPATCGATTACGAGAGGTGGCAAGCAACCAATTCGTGAAACGAACATCTACATGTAAT 4680
Db 4681 tatattcgtattcttcatcatattgactcttttccacactcaatctgttcattggtg 4740
Qy 4681 TATATTTCTGTATCTTTCATCATATTTGGATCCTTTTTCACATCAATCTGTTTCATTGGTG 4740
Db 4741 ttcatcttgataattttaatgagcaaaagaaagcaggttgatcatattagaatttca 4800
Qy 4741 TTATCATTTGATAATTTAATAGCAAAAGAAAAAGCAAGAGTGGATCAATTAGAAATGTTCA 4800
Db 4801 tgcagaagatcagaaaaagtactataatgctatgaaaaagatgggctcttaaaaaaccat 4860
Qy 4801 TGACAGAAATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860
Db 4861 taaaagccattccaagaccaaggttggcgaccacaagcaatagtcttgaataagtaacgg 4920
Qy 4861 TAAAAGCCATTCCAGACCACAGGTGGCGACCAACAGCAATAGTCTTTGAAATAGTAACGG 4920
Db 4921 ataagaaattcgataaatcattattgtttatttcatttgggtgtgaacatgtttccaccatgaacc 4980

Qy 4921 ATAGAAATTCGATATAATCATATTATGTTATTCATTGGTCTGAACATGTTACCATGACC 4980
Db 4981 tcgatcgttaacatgctcggacacgtataacgcggtccctagactatctcaatcgtatat 5040
Qy 4981 TCGATCGTTAGATGCGTCCGACACGTATAACCGGGTCCCTAGACTATCTCAATCGGATAT 5040
Db 5041 tclagttattttcagttcccgaatgctattataaaaaatttcgctttacgatatcacatt 5100
Qy 5041 TCSTAGTATTTTCAGTTCGGAATGCTATTAAAAATATTCGCTTTAGGATATCACATATT 5100
Db 5101 ttattggccatggaatttatttgatgtagttagttgtoattttatccatcttaggtcttg 5160
Qy 5101 TTATTGAGCCATGAAATTTATTGATGAGTAGTGTTCATTTATTCATCTTAGTCTGTG 5160
Db 5161 tacttagcgatatattcgaagaagtacttcgtgcgcgaacctctccgaatggtgctg 5220
Qy 5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCCGCGACCTGCTCCGAGTGGTGCTG 5220
Db 5221 tggcgaagtgggcgctgctccttcgactggtgaaggggagccaaaggcattcggacactgc 5280
Qy 5221 TGGCGAAAGTGGCGCTGCTTCGACTGGTGAAGGGAGCCCAAGGGCATTTCGGACACTGC 5280
Db 5281 tcttggogtggccatgtcgtcgcggccctgttcaacatctcgtcgtgttctctctg 5340
Qy 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCCCTGTTCAACATCTGCTGCTGTCTCTCTG 5340
Db 5341 tcatgttcatctttgcccattttcgccatgtcgttcttccatcagctgaagagaagacg 5400
Qy 5341 TCATGTTTCATCTTTGCCATTTTCGCATGTCTGCTTTCATGCAGTGAAGGAGAAAGCG 5400
Db 5401 gcattaaacgagctctcaacttcaagaccttggccagagcatatcctcgtctcttcsaga 5460
Qy 5401 GCATTAACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCCTCTTTTCA 5460
Db 5461 tgcgaacgcagcgggttggatggttactcggagccattatacaatgagagaacatcg 5520
Qy 5461 TGTCGACCTAGCGGTTGGGATGGTACTTGGACGCCATTATCAATGAGGAAGCATCG 5520
Db 5521 atccacccagcagcaaaagctatccggcaatttggttcagcgaccttgaataaa 5580
Qy 5521 ATCCACCCGAGCAGCAAAAGCTATCCGGCAATTTGGTTTCAGCGACCTGTTGAATAA 5580
Db 5581 cgttctcctctcatccctagttataagctttttgatagttataatgtacattgctg 5640
Qy 5581 CGTTTCTCTCTCATACCTACTTATAAGCTTTTTCATAGTATTATTAATGTATCATTTGCTG 5640
Db 5641 tcatcttcgaaactatagtcaggccaccggagcgtgcaaggtgtcaaggggtctaaccgacg 5700
Qy 5641 TCATTTCTGAGAACTATATAGTCAGGCCACCGAGGACGTCAAGAGGGTCTAACCCGACG 5700
Db 5701 actcagacatgactatgagatcggcagaattcogattccggagggcaccagttacatac 5760
Qy 5701 ACTAGCATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCAGTACATAC 5760
Db 5761 gctatgacagctgtcccgaattcctggagctactggagcccccgctgcagatcccaaac 5820
Qy 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCGCTGCAGATCCCAAA 5820
Db 5821 cgaacaagtaacaagatacatatcgatggacatacccatctgtcgcggtgacatcgtact 5880
Qy 5821 CGAACAAAGTACAAGATCATATCGATGGACATACCATCTGTCGCGGTGACCTCATGTACT 5880
Db 5881 gctgcgacatcctcgacgccccttcgaagaacttcttgcgcgaagggcgaatccgatac 5940
Qy 5881 GCGTCGACATCTCTGACGCCCTTACGAAGACTTCTTTTCGCGGGAAGGGCAATTCGATAG 5940
Db 5941 aggcagcgggtgagattggtgagatagcggccccgcggatcacgagggctacgagccg 6000
Qy 5941 AGGACACGGGTGAGATTGGTGAATAGCGCCCCCGCCGGATACGAGGGCTACGAGCCCG 6000
Db 6001 tctcatcaacgctgtggcgtcagcgtgaggagtactgcgcgcgggctaataccagcaacgctt 6060

5144 ATCCATCTAGTCTGTACTTACGATATTATCGAGAAGTACTTCGTGTCGCCACCT 5203
 5064 cttccgggtatccctctgcccagatcggccgatctccatcagctgataccggggagca 5123
 5204 GTCCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 5263
 5124 ggggattccgacgtctctcgcctcctgatgtccctcgcgcgcctctcaacatcgg 5183
 5264 GGGCATTCGGACACGCTCTTCGCTGGCCATGTCGCTGGCCGCTTCGCTTCACATCTG 5323
 5184 cctcctcctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5243
 5324 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5383
 5244 cgtcaagtggagggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcgg 5303
 5384 CGTGAAGGAGAGAGCGGCAATTAACGAGCTTACAGCTTCAAGCTTTCGTCAGAGCAT 5443
 5304 gctgtgctgttccagataccacacacacacacacacacacacacacacacacacacac 5363
 5444 GATCTGCTCTTTCAGATGTCAGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 5503
 5364 caacacggggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5423
 5504 CAAT--GAGGAAGC--A-TGCGATCC--ACCCGAC-AGCGACAAGGCTATCCGGCAA 5554
 5424 cgtgtggagccggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcgg 5483
 5555 TTGTGGTTCAGCGACCGTGGGAATACGTTTCTCTCTCATACCTAGTATTAAAGCTTTT 5614
 5484 catcgtgtcaacatgtacatcgcctcctcctcctcctcctcctcctcctcctcctcct 5543
 5615 GATATTATTATATATGATATGCTGCTATTCGAGAACTATATGTCAGGACCCAGGA 5674
 5544 gaggcacagccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5603
 5675 CGTGAAGAGGGTCTAACCGAGCGAGCTACGACATGATGATGATGATGATGATGATGAT 5734
 5604 gacccggagggcaccagctcctcctcctcctcctcctcctcctcctcctcctcctcct 5663
 5735 CGATCCGAGGGACCCAGTATACGCTATGATGATGATGATGATGATGATGATGATGATG 5794
 5664 gctcagccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5723
 5795 GGAGCCCGCTGCAGATCCAAACCGAAGTACAGATCATATGATGATGATGATGATGATG 5854
 5724 catggtgagcggagaccgtatccatcctgtaggacatctgttcgttccaccaa 5777
 5855 CATCTGTCGGGTGACCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5908

RESULT 4

ID Q05831 standard; cDNA; 7555 BP.
 AC Q05831;
 DT 10-JAN-1991 (first entry)
 DE Cardiac sodium channel gene.
 KW Rat; arrhythmia; ss.
 OS Rattus rattus.
 PN W09009391-A.
 PD 23-AUG-1990.
 PR 09-FEB-1990; U00768.
 PR 13-FEB-1989; US-310330.
 PA (ARCH-) ARCH DEV CORP.
 PI Rogart RB;
 DR WPI; 90-275095/36.
 PT New rat cardiac sodium channel proteins - and associated DNA
 PT sequences, polypeptides and peptides associated with
 PT proteins, useful as antiarrhythmic and cardiotoxic drugs.
 PS Claim 7; Fig 1; 65pp; English.
 CC The sequence is derived from 3 overlapping clones, PRH3-1, PRH4-23,
 and PRH14-31. (Deposited as ATCC 67885, 67886, and 67887 resp.)

The clones were isolated from a cDNA library in the lambda zap
 vector prepd. from mRNA obtd. from newborn rat hearts using rat
 brain II cDNA probe. The isolated DNA can be used to screen a
 similar human derived cardiac cDNA library for the corresponding
 human gene. Proteins produced by expression of the DNA have
 diagnostic therapeutic, and prognostic applications.
 Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;

Query Match 5.3%; Score 344; DB 1; Length 7555;

Best Local Similarity 63.3%; Pred. No. 2.17e-213; Indels 30; Gaps 19;

Matches 1174; Conservative 0; Mismatches 650;

3927 ggacaagatgtccactacgtcttgtgtgagatgtctcaagtgggtggcctacgg 3986

4082 GGACAGATATTACGGTTATATCTTCTGGAAATGTTAATCAAGTGTGGCGCTCGG 4141

3987 cttcaagaagtacttcccaacgcctgtgtgtggtgacttctctgttggagctctc 4046

4142 CTTCAAAGTACTTACCAACGGGTGTTGGTCTGATTTCTGATTTGTCATGTTATC 4201

4047 gctggtcagcctcgtggcacaacaccttagcttgcgcgaatgggtcccatcaact 4106

4202 GCTTATCAACTTCGTTGCTTTCACTTGTTGGAGTGGTGTATTCAGGCTTCAAGAC 4261

4107 gagacactgcgtgcacttcgacctcagccctcagggccttctgcagatttggagc 4166

4262 CGGACGTTAAGACACTGAGACCACCTACGTGCCATGTCCTGATGCGAGGCATG 4321

4167 ggtggtcaatgcgtgtgtgggcccacccccctccatcctatgaacgtcctcctc 4226

4322 CGTCTTAATCGCTGGTACAAGCTATACCGTCCATCTTCAATGCTGCTATTGGTGT 4381

4227 catctctcgtcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 4286

4382 AATATTTTGGCTAATTTTGGCCATTAATGGGTGTACAGCTTTTGTGCTGAAATAT 4441

4287 gtgcatacaccagacagaaggggacctcctcctcctcctcctcctcctcctcctcct 4346

4442 GTGCGAGGAC--AT-GAATGCGACGAAGCTCAGC-C-ACGAGATCATACCAAT 4495

4347 tgaatgagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 4406

4496 TGCTGCGAGAGCGAGAAC-T-ACAGGTGGGT-GAATTC-AGCAA--TGAATTTTGA 4546

4407 tgaacagtggagcgggtacctcctcctcctcctcctcctcctcctcctcctcctcct 4466

4547 T--CAT-GTAGTAACGGTATCTGTGCTTTTCCAGTGGCCCTTCAAGGCTGGAT 4603

4467 ggacatcatgtatgcgtgtggactccagaggggtatgaggagcagcgcagtggaaga 4526

4604 ACAATCATGAACGATGCTATCGATTACGAGAGGTGCAAGCAACCAATTCGTGAAC 4663

4527 caacctctacatgtacatctacttctcctcctcctcctcctcctcctcctcctcct 4586

4664 GAACATCTACATGATTTATATTTCTGATTTCTCATCATATTTGGATCTCTTTTCACT 4723

4587 caacctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 4646

4724 CAATCTGTTTCATTTGTTGTTATTTTAAATGAGTAAATTTTAAATGAGTAAATTTTAA 4783

4647 c-cag--gatatcttcacgtgagcagagaagactactacaatgcatgaagaagct 4703

4784 ATCATTTAGAAATGTCAGAGAGATCAGNAAAAGTACTATATGTTATGTAAGAAAG 4843

4704 ggggtcccaagaaacccccagcccatccccagcggccttgaacaaagtcaccaggtttcat 4763

4844 GGGCTCTAAAAAACCATTTAAAGCCATTTCCAGACCAAGGTGGCGACCAACCAATAGT 4903

4764 attcagacattgtaccagcagcggcctcctcctcctcctcctcctcctcctcctcct 4823

4904 CTTTGAATAGTAAACCAAGAAATTCGATATATCATATGTTATTTCATTTCGTTGAA 4963

4824 catggtgaccatgatggtggagacagatgaccagagccctgagaaggtcaacatctggc 4883

RESULT 5
m30103 standard: cDNA: 3033 BP.

Borden LA, Halegoua S, Mandel G;
WPI; 96-251547/25.
DR P-PSDB; R99639.
DD Nucleic acid encoding peripheral nervous system specific sodium
PT channel peptide - useful for sodium channel-associated disease or
PT trauma.

Example 1; Fig 9: 80pp; English.
PS The sequence encodes "a rat peripheral nervous system sodium channel
CC peptide-1 alpha-subunit (PNI) with sodium channel activity, and
CC has been isolated from a rat PC12 subclone PKI-4 cell culture,
CC expressing high levels of cAMP-dependent protein-kinase-inhibitor.
CC A CDNA library has been screened with primers T30196-97, and the
CC product has been used as a probe to re-screen the library to
CC isolate the fragment given in T30192. This has been used to isolate
CC the full-length gene. A probe derived from the sequence may be
CC used in differential tissue expression studies. The peptide may be
CC used to isolate sodium-agonists and sodium-antagonists for use as
CC analgesics, hypotensives, antiinflammatories, and in therapy of
CC sodium channel-associated pathology or trauma, e.g. neurological
CC disorders. The DNA (in sense or antisense orientation) may be used
CC in gene therapy.
CC Sequence 6452 BP; 1816 A; 1454 C; 1550 G; 1632 T;
SQ

Query Match 4.8%; Score 312; DB 22; Length 6452;
Best Local Similarity 62.3%; Pred. No. 8.04e-191;
Matches 1210; Conservative 0; Mismatches 700; Indels 33; Gaps 21;

Db 3920 atgatctcgtccagcagtggagctcggtgtttgaagatatcatattgaaagaagaag 3979
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3996 ATGATTTTAATGAGTAGCTTACGTGGCATTAAGAAGATGATCACTGCCACAAGACC 4055
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3980 accattaagattatctcaggatgtagtgcacagatattcaactacattcttcattcgtaa 4039
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4056 ATACTCGAGGATATTATTACTATATGNCAGATAATTACGGTTATATCTTCCTTGAA 4115
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4040 atgtctctaataatgggtcgcatatgggttatataaacatatattcattaatgctggttg 4099
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4116 ATGTTAATCAAGTGGTGGCGCTGCCTTCAAAGTGTACTTACCACCGCTGGTGTGG 4175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4100 ctggacctttaatttgtatgtgtctctagttaatttagtagccaactcttggctac 4159
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4176 CTCGATTTCGTGAATGTTCATGTTNCGCTTATCAACTTCGTGCTTCACTTGTGGAGCT 4235
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4160 tcgaccttggccccattaaatctctacggacactgagggcccttaagacccttaagagcc 4219
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4236 GG TGATTTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTGAGACCCTACTAGTCCC 4295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4220 ttgtctagatttgaagaatgagggtagtggctcaacgactcataaggagacaatcccctcc 4279
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4296 ATGTCCCGATPGCAGGCCATGAGGGTCGTGCTTAATGCGCTGGTACAAGCTATACCGTCC 4355
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4280 atcatgaacgtgctctctcgtgctctattctcgtctaattatttagcatatgagagtc 4339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4356 ATCTTCAATGTCTATTGGTGTGCTAATAATTGGCTAAATTTTGCCTATATGGGTGTA 4415
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4340 aaatctgttgtggcaagttctatgagtgtgtcaacaccacgcatgggttcagattccct 4399
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4416 CAGCTTTTTTGTGGAATAATATTTTAAGTCGAGGACATGA---ATGG--CACGAAGCTCA 4470
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4400 acatctcaagttgcaaacgcttcgtgagtggttttccctgntgaacgttagtggaagtgtg 4459
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4471 GC-CACGAGATCATACCAATCGCAATGCCT-GC----GA-GACGGAGAACT-ACAGGTG 4522
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4460 cgatggaaaaaacctgaagtaaaccttcgaacagcttggcttggttacctcgtcgtgctt 4519
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4523 GG-TG---AATTCAGCAA-TGAATTTTCGATCATGTAGTAACGGGTATCTGTGCGCTTTC 4577
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4520 caagttgcaacattcaaagggctggatgatattatgtatgcagcagttgactctgtaaat 4579
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4578 CAAGTGGCCACCTTCAAAGCGCTGGATACAAATCATGAACGATGCTATCGATTACGAGAG 4637
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4580 gtaaatgaacagccgaaaatacgaatacacgtctctcatatgataatttacttctgcatcttc 4639
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT	8	
ID	T30195 standard; CDNA; 6404 BP.	
AC	T30195;	
DE	25-OCT-1996 (first entry)	
DT	Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.	
DE	Human; peripheral nervous system; sodium channel; PN1B;	
KW	dorsal root ganglion; sodium-agonist; sodium-antagonist;	
KW	drug screening; analgesic; hypotensive; antiinflammatory; trauma;	
KW	pain; neurological disorder; antisense; gene therapy; ss.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	49..6015
FT	/*tag= a	
FT	/product= PN1B protein	
FT	misc_difference 334..336	
FT	/*tag= b	
FT	/codon= seq:ACA, aa:Ala	
FT	misc_difference 1738..1740	
FT	/*tag= c	
FT	/codon= seq:ATA, aa:Leu	
FN	W09614077-Al.	
PD	17-MAY-1996.	
PP	02-NOV-1995; U14251.	
PR	02-NOV-1994; US-334029.	
PR	07-JUN-1995; US-482401.	

Query Match	4.7%;	Score 308;	DB 221;	Length 0467;
Best Local Similarity	62.2%;	Pred. No. 5,266-188;		
Mismatches	0;	Mismatches 713;	Indels 35;	Gaps 25;
Matches	1231;	Conservative		
3614	ttgaacacagttggttgaagcttcattgttctcatgatctctcagcagtggtgtccc	3673		
3961	TTGAAAATAAATATTTTGAACAGCGTGTATCAGTATGATTTTAAAGTAGTAGCTT	4020		
3674	tggcttttgaagattattattgaaggaacacccaattgaattatctctggagtatg	3733		
4021	TGGCATTAGAGAGATGACATCTCCACAAAGACCATACTGCAGGATATTTTATAC	4080		
3734	cagacaagatcttccactacattctcattctggaaatgctctcaaaaggatagcatatg	3793		
4081	TGGACAGAAATTTACGGTTATATCTTCTTGAAATGTTAATCAAGTGGTGTGGCGTCG	4140		
3794	gttataaacatattcaccaatgcctgggttggctggattctcctaattgttgatgttt	3853		
4141	GCTTCAAAGTGTACTTACCACACGCGTGGTGGTCGATTCGTGTGATGTGCATGGTAT	4200		
3854	ctttggttacttttagtgggcaaacactcttggtactcagatcttggccccaataaacc	3913		
4201	CGCTTATCAACTTCGTTGCTTTCACCTTGTGGAGTGGTGTATTCAGGCTTCAAGACTA	4260		
3914	ttcggacactgagagctttaagacctctaagagccttatctagatttgaagaaatgaggg	3973		
4261	TGGGAACGTTAAGACACTGAGACCACACTAGTGCATGTCCGTATGCAGGCGATGAGG	4320		
3974	tctgttgatgcactcataggagcaatctctccatcatgaatgctactgtgtgtc	4033		
4321	TCGTCGTTAATCGCTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGCGTGTGC	4380		
4034	tatatcttgctgatattcagacatcaggagtaaatttgttctggcgcaagtcttatg	4093		
4381	TAATATTTTGGCTTAAATTTTGCCATANTGGGTGTACAGCTTTTGTGCGAAATATTTTA	4440		
4094	agtgtattaacacacacagatgggtcacgggttctctgcagtcagttcccaaatcgttccg	4153		
4441	AGTCGGAGGACATGATGTCACGA-A-GCTCAGCCACGAGATCA-TACCAATCG---C-	4493		
4154	aatgttttgccttatgaatgttagtcaaaatgtcgtatggaaaaacctgaaagtgaact	4213		
4494	AATGCCP-GGG---A-GAGCGAGAA-CTACAGTGGG-TG---AATTCAAGCAA-TGAATT	4542		
4214	ttgataatgtcggaacttggttacctatctctcttccaaagttgcaccttttaaggagatga	4273		
4543	TGATCATGTAGGTAAACCGCTATCTGTGCTTTTCCAGTGGCCACCTTCAAGAGCTGGA	4602		
4274	cgattattatgtatgcagcagtgattctgttaatgtagacaagcagcccaaatatgaat	4333		

QY 4603 TACAAATCATGAACGATGCTATCGATTACAGAGAGGTGACGAAGCAACCAATTCGTGAA 4662
Db 4334 atagcctcaatgatatatttatttgcgtctttatcatcatcttgggtcattcttcactt 4393
QY 4663 CGAACATCATCATGTATATATATTCGTATTCATCATATTCATTCATTCATTCATTC 4722
Db 4394 tgaactgttcatgtgtcatcatagataatttcaacacacagaa-aaagaagtgtga 4452
QY 4723 TCAATCTGTTTCATGTGTTTCATGTATATTTTAATGAGCAAAAGAAAGCAGGTG 4782
Db 4453 ggtca--agacatctttatgacagaagaacagaatactataatgaatgaaaaagc 4510
QY 4783 GATCATTAGAAATGTTTCATGACAGAAGATCAGAAAAGTACTATAATGCTATGAAGA 4842
Db 4511 tggggtccaaagaagccaaagcaattcctcgaccagggaacaaaatccaagtata 4570
QY 4843 TGGGCTCTAAAAAGCATTAAGCCATTCCAAGACCAAGGTGGCGACCAAGCAATAG 4902
Db 4571 tatttgacctagtgacaaatcaagcctttgatatttagtatcatgtgttcttctctca 4630
QY 4903 TCTTTGAATAGTACCGATAGAATTCGATATAATCATATATGTTATTCATTCGTCTGA 4962
Db 4631 acatggttaacctatggttagaagaagggggt- caaagtcaacatatgactgaagttaa 4689
QY 4963 ACATGTTCCACCATGACCCCTCGATCGTTACGATCGCTCGACACGATATAAC-CCGTCCTA 5021
Db 4690 tattggataaattggtttttataatccttttcaatggaagaatggtgctaaactgac 4749
QY 5022 GACTATCTCAATGCGATATTCGTATTTTCAGTTCGGAATGTTCTATTAATAATATTC 5081
Db 4750 tccctcagacactactactcaacttagtagtggaataatttttgatttgggtgttgatt 4809
QY 5082 GCTTTACGATATCATATTTATGAGCAAGGAATTTATTTGATGTAGTAGTGTCTATT 5141
Db 4810 atctccattgagtgattgtttctagctgattgattgaacgattttgtgtccctacc 4869
QY 5142 TTATCCATCTTAGGCTTGTTACTTAGCGATATTATCGAAGTACTGCTGTGCGCGACC 5201
Db 4870 ctgttccagagtagatcgctctgceaggattggccgaatcctcactgctgaagaagaca 4929
QY 5202 CTGCTCCGAGTGGTGGTGCGGAAGTGGCGCGTGCCTTCGACTGGTGAAGGGAGCC 5261
Db 4930 aagggtatccgcacgctgctgttctgttgatgctgctcctcctgctgtgtttaacatc 4989
QY 5262 AAGGCAATTCGGACACTGCTCTTCGGTGGCCATGTCGTCGCGCCCTGTTCAACATC 5321
Db 4990 ggcctcctgctcttccctggtatgctatcctacgcacatcttgggaatgtccaaacttgcc 5049
QY 5322 TGCCCTGCTGCTGCTGCTGCTATGCTATCTTTCGCTATTCGCGATGCTGCTCTCATG 5381
Db 5050 tatgttaaaaagggaatggaatgaatgacatgttcaattttgagacctttggcacaagt 5109
QY 5382 CAGGTGAGGAGGAAGAGGGCGATTAACGACGCTACACACTTCAAGACCTTTGGCCAGAGC 5441
Db 5110 atgatttgctgttccaaattacaacctctgctggtgggtgattgcttagcacctatt 5169
QY 5442 ATGATCCTGCTCTTTTCAGATGTCGAGTTCAGCGGTGGGATGGTGTACTGGACGCCATT 5501
Db 5170 cttacagtaagccaccgactgtgaccccaaaaaaagtctcctcctgggaagttcagttgaa 5229
QY 5502 ATCAATAGGAAGCATGCGA-TCC-ACCGACAGC-GA-CAAAAG-GCTA--TCCG--G-- 5550
Db 5230 ggaagactgtgtaacccactgttggaaattcttacttctgttagttatcatcatatcc 5289
QY 5551 GCA-ATGTGGTTCAGCGACCGTGGGAATGAAGTTTCTCCTCTCATACCTAGTTATAAGC 5609
Db 5290 ttccgtggttggtaaacatgtacattgcagtcatactaggagaatttttagttgtccact 5349
QY 5610 TTTTGTATAGTTATTAATATGTACATGTGCTGTCATCTTCGAGAACTATAGTCAGGCCACC 5669
Db 5350 gaagaaagtactgaacctctgagtgaggtgactttagatgttctatgaggtttggag 5409

RESULT

ID Q71202 standard; DNA; 2308 BP.

AC Q71202;

DT 11-MAY-1995 (first entry)

DE scd131, a subclone of hscpl, encodes a non-dipteran sodium channel.

KW non-dipteran sodium channel; lepidoptera; insecticide; sensitivity;

KW target site: pyrethroids; marker; resistance; probes; detection;

KW PCR; polymerase chain reaction; Heliothis; degenerate;

KW Drosophila melanogaster; homologue; hspcl; para locus; scd13; ss.

OS Heliothis virescens.

FH Key Location/Qualifiers

FT intron 169

FT /*tag= a "end of putative intron"

FT /note= 170..292

FT /*tag= b "putative exon"

FT /note= 293..388

FT /*tag= c "putative intron"

FT /note= 389..583

FT /*tag= d "putative exon"

FT /note= 584..679

FT /*tag= e "putative intron"

FT /note= 680..923

FT /*tag= f "putative exon"

FT /note= 924..1252

FT /*tag= g "putative intron"

FT /note= 1253..1523

FT /*tag= h "putative exon"

FT /note= 1524..1607

FT /*tag= i "putative intron"

FT /note= 1608..1912

FT /*tag= j "putative exon"

FT /note= 1913..2095

FT /*tag= k "putative intron"

FT /note= 2096..2308

FT /*tag= l "putative exon"

FT /note= 170..2308

FT CDS

FT /*tag= m misc_feature 2107

FT /*tag= n "any of T,C,G or A"

FT /note= 2158

FT /*tag= o "either T or C"

FT /note= 2203

FT /*tag= p "any of A, T, G, or C"

QY 5670 GAGGACGTGCAAGAGGGTCTAACCGACGACGACTACGACATGTACTATGAGATCTGGCAG 5729
Db 5410 aagtttaaccgagatgagccaggtttatagagttctctaaactctctgatttgcagct 5469
QY 5730 CAATTCGATCGGAGGCGACCCCATACATACGCTATGATCAGCTGTCCGAATTCCTGGAC 5789
Db 5470 gccctggatcctctctctctcatagcaaaaccccaaaagtcacagctcattgcccattgat 5529
QY 5790 GTACTGGAGCCCCGCTGCAGATCCACAAACCGAACAGTACAAAGATCATATCATGGAC 5849
Db 5530 ctgcccattggttagtgtagccgagatccattgtcttgaacatcttattgtctttacaaa 5588
QY 5850 ATACCCATCTGTCGGGTGACCTCATGTACTGCTCGACATCTCTCGAGCCCTTACGAA 5908

[illegible]

Tue Oct 14 14:18:08 1997

```
FT Modified-site 600..602
PN /label-N-glycos_site
PD W09100292-A.
PF 10-JAN-1991.
PR 22-JUN-1990; U03586.
PA (GETH ) GENENTECH INC.
PI Chang M, Goeddel D, Lowe D;
DR WPI; 91-036711/05.
DR N-PSDB; Q10324.
PT Natriuretic protein receptor B - for diagnosis and treatment of
PT kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
PS Claim 3; Fig 1; 49pp; English.
CC The sequence was derived from the DNA encoding natriuretic peptide
CC receptor B, NPRB, having guanyl cyclase (GC) activity and protein
CC kinase activity. The DNA can be inserted into expression vectors
CC for the prodn. of the protein, opt. after being mutated to produce
CC NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
CC 114,952). The protein (or variants) can be used in treatment of
CC natriuretic peptide disorders, and also to isolate peptides using
CC affinity chromatography. Antibodies with affinity for NPRB can
CC also be prep'd.
SQ Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;

Query Match 1.3%; Score 86; DB 2; Length 1047;
Best Local Similarity 8.7%; Pred. No. 8.70e-36;
Matches 86; Conservative 279; Mismatches 619; Indels 10; Gaps 10;

Db 1 mannsnnnnvnaagvrrngarnntnnavnnnnhnsyavawrvrgnavananganran 60
Cp 2894 CATCACCGAAGATGAAGATGATAATGCAAGATACAAATGTCAGATTACCCAAAGCGCC 2835
Db 61 nvdrnrvsnngacsnynannasvdknxyhdndnnngvcyynasvwnash-wrnnn 119
Cp 2834 CATGGTCCTCCCAATCGAATAGTAAATAGTAAATAGTGGGCCCAAGACTGGCCAGTTT 2775
Db 120 ntagavasnakndhyrtnvrtgnsankngnnvtnhgnnwtaaraannndartddrn 179
Cp 2774 GAATACCCAGCAATCGAAAGGACGCAATACGACAGACCCCTGGACACCTCGAGTCC 2715
Db 180 hyatngvnnangsnsvnhvnyarnngnnnathnr-angrnrvncngnnnnnnnnnn 238
Cp 2714 CAGTTCCAATAGCATGAGGCGCACGATATGAGTTCGAAGATGTTCCAGCCCTCTCGAA 2655
Db 239 naarnntagdyvnyndvngnsnragtnratgrvndntrnnanrnanntnvnnty 298
Cp 2654 ATAGTACTTGGGCTCATGCCCATAGCTTCATGCTCATGCTGCTGCTGCTGCTGCTGCT 2595
Db 299 rnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 358
Cp 2594 GAAGAAATAGTTCGCACTCTTGAGCACGCGGTTCCATCTCTTGTTCATATCGTGTGATC 2535
Db 359 ndgnrvnmkgrryhgvtgnyvmdkndndntdnvngdndsgdnnaahysganknn 418
Cp 2534 CATTCGCATGAACATCTGTTGACCAATGACATGACACCGCTGATGAAGAGTCCGACGAGG 2475
Db 419 wwtgrnnnwkgannsdnnncandndndscdktnnstnanvngtntnmmngvsnnnnn 478
Cp 2474 ATCGAAGCATGAGCGCATACCCACT-CCTGAAATTTCAACCAAAACCCAGCAACAGTCCC 2416
Db 479 rkmmnnknaasmvnrnnnnnnngsnryhkgagstntnsnrgssygsnmtahgkyinna 538
Cp 2415 ACACACAAAACATCATGATGCTTTGAGGATCACTTCGAGTG-CCTTGCTTTGACGTC 2357
Db 539 ntghkgvrvvankhvkrrnntrnnvnnnnkhmrdrnnnnhntnngacndnnnnnntvny 598
Cp 2356 G-GCCATCTCTCGTCATCGTCTCTGTTGGAAATAGTAAACGAGAG-ACCG-CGATCG 2300
Db 599 cnrgsnndnnnnndnnmrynnndrvkgnannhnsnshgnsksncvvdsvrva 658
Cp 2299 CTTGCCCCGACTGTGCGGACGAGCGCTGTTGATGATGATGATGATGATGATGATGATGAT 2240
Db 659 kntdygnasnrs-tannndnnnnyaknntannnnnnnnnnnttgmnaadvysngnnnnna 718
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Cp 2239 TTCAATCAACACCGCTTTGTGTCGACGGGCTCGATAAAGATTGTGCATGATTTTA 2180
Db 719 nrsgnynngndnshknvknvngnrvnrsndntnnnnnnnnnnnnnnnnnnnnnnnn 778
Cp 2179 ATCTGTGCAGCTTCGTCGTCGAC-T-CCAGGCCAATTTCGTAGTCGCGATGATCGAGCT 2122
Db 779 ngnnkgnrrnnknggtsnndnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 838
Cp 2121 TGTGATTGGTGTCCAGACAGTGTGCGCCCATTTGGTGGCGCC-CACTGATTGATTGCGT 2063
Db 839 nhsvannnnkrgntvnanandsvtvnyndvntansanstnmvntnnnnnnnnnnnnnn 898
Cp 2062 GTGTGCGGTTGCGCAATTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2003
Db 899 ndvkvntngdaymvyvsgnngnrgnchnannanmanannavsnrnrhnrhnnnnnn 958
Cp 2002 CCGCGGAGTAGTCCCATGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 1943
Db 959 gyhtgnvcagvvgknmrycngngdvtntasrms 992
Cp 1942 GAGTGTGGGAGCCTAGATTGCCATAGTACACGG 1909
```

```
RESULT 13
ID N81164 standard; DNA; 204 BP.
AC N81164;
DT 08-NOV-1990 (first entry)
DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS Escherichia coli.
FH Key Location/Qualifiers
FT misc_feature 19..69
FT /tag= a
FT /function-multiple cloning site
FT primer_bind 187..204
FT /tag= b
FT EP-285123-A.
PN 05-MAY-1988. 105163.
PR 30-MAR-1988; US-034819.
PR 03-APR-1987; US-034819.
PA (SUSO) SUOMEN SOKERI OY.
PI Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T;
WPI: 88-279927/40.
DR Introducing random point mutations into nucleic acids -
PT by prep'n of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PS Disclosure; p; English.
CC Random point mutations were introduced into the alpha fragment of
CC E.coli beta-galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a pop'n of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC transcriptase and the molecules are completed to forms that can be
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 diff base substitutions, most of which
CC occurred singularly in any given mutant.
CC See also P80575.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 0.8%; Score 50; DB 1; Length 204;
Best Local Similarity 17.2%; Pred. No. 1.59e-13;
Matches 21; Conservative 63; Mismatches 36; Indels 2; Gaps 2;

Db 78 dchvgcgcygmttt-hhyrrmrbnvdyrdnsdaawyc-cyrsvkydcynachhddh 135
Qy 5722 TCTGCGACCAATTGATCCGGAGGCGCACCCAGTACATACCTATGATGATGATGATGATGAT 5781
Db 136 vvybbvnyvnhnncncbnnhvhvbnhnnhnnvnyvnyvnyvnyvnyvnyvnyvnyvny 195
Qy 5782 TCCTGGAGCTACTGGAGGCCCGCCGCTGCGAGATCCACAAACCGAACAGATCATAT 5841
```

[illegible]

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WQSRLE

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat Oct 11 03:30:08 1997; MasPar time 3303.72 Seconds
Tabular output not generated. 1011.963 Million cell updates/sec

Title: >US-08-554-424-7
Description: (1-6513) from US08554424.ssq
Perfect Score: 6513
N.A. Sequence: 1 TCTAGAGCTTGGCGCATAG.....ACGCGAGTATTAGCTTAGA 6513
Comp: AGATGTCACCGCGCATC.....TGGCICATATGAGATCT

Scoring table: TABLE default
Gap 6

Mismatch STD : Dbase 0; Query 0

Searched: 707517 seqs, 256659390 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
1:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
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195:EST195 196:EST196 197:EST197 198:EST198

Statistics: Mean 12.713; Variance 2.153; scale 5.904

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	124	1.9	343	107	HSC2HD061	H. sapiens partial cD 5.78e-208
2	30	0.5	147	138	AA047504	zK73C04.r1 Soares pre 2.16e-12
3	32	0.5	174	121	W55354	mb13B03.r1 Life Tech 1.83e-15
4	31	0.5	179	109	HS046448	Human EST overexpress 6.54e-14
5	30	0.5	279	82	H31486	EST105554 Rattus sp. 2.16e-12
6	31	0.5	285	34	R1C1140A	Rice cDNA, partial se 6.54e-14
c 7	30	0.5	309	135	SSV11C2	S.scrofa mRNA (clone 2.16e-12
8	31	0.5	315	70	H79476	yu49a03.s1 Homo sapie 6.54e-14
c 9	32	0.5	323	176	W91417	mr85a01.r1 Soares mou 1.83e-15
c 10	32	0.5	352	187	AA145456	mr10B01.r1 Soares mou 1.83e-15
c 11	32	0.5	355	142	HS278350	H. sapiens mRNA, expre 4.80e-17
c 12	32	0.5	356	134	AA168787	ms36B04.r1 Stratagene 1.83e-15
c 13	30	0.5	359	109	HS047708	Human EST overexpress 2.16e-12
c 14	34	0.5	374	187	AA144007	mr75B01.r1 Stratagene 1.17e-18
c 15	32	0.5	389	109	HS046419	Human clone xs430 mRN 1.83e-15
16	30	0.5	391	122	W62722	md82h10.r1 Soares mou 2.16e-12
c 17	32	0.5	400	104	N75422	zs82f02.s1 Homo sapie 1.83e-15
c 18	31	0.5	407	11	T96117	ye48B03.s1 Homo sapie 6.54e-14
c 19	34	0.5	409	190	AA153254	mr77C01.r1 Stratagene 1.17e-18
c 20	34	0.5	419	109	HS278350	H. sapiens partial cD 1.17e-18
c 21	30	0.5	424	27	N59836	yh11f05.r1 Homo sapie 2.16e-12
c 22	32	0.5	438	91	R28668	yx58B09.r1 Homo sapie 1.83e-15
c 23	30	0.5	439	119	W45922	mc79A03.r1 Soares mou 2.16e-12
c 24	30	0.5	441	162	AA102073	z179A06.s1 Stratagene 2.16e-12
c 25	34	0.5	443	142	HS278389	H. sapiens mRNA, expre 1.17e-18
26	31	0.5	455	18	T51846	yB54f01.s1 Homo sapie 6.54e-14
27	30	0.5	458	190	AA154617	ms17e10.r1 Stratagene 2.16e-12
c 28	32	0.5	473	2	T61453	yc06e10.s1 Homo sapie 1.83e-15
c 29	30	0.5	474	177	AA061573	ms38P08.r1 Soares mou 2.16e-12
30	30	0.5	528	137	AA173765	zP30A07.s1 Stratagene 2.16e-12
c 31	30	0.5	534	190	AA153188	ms62e10.r1 Stratagene 2.16e-12
c 32	32	0.5	542	163	AA111051	mp62d11.r1 Soares 2Nb 1.83e-15
c 33	30	0.5	577	116	W27397	28e1 Human retina cDN 2.16e-12
c 34	32	0.5	593	196	AA170896	ms49f07.r1 Life Tech 1.83e-15
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36	30	0.5	782	142	HS278311	H. sapiens mRNA, expre 2.16e-12
37	30	0.5	880	159	AA036217	mr17402.r1 Soares mou 2.16e-12
38	29	0.4	165	166	SSC11D08	S.scrofa mRNA; expres 6.59e-11
39	29	0.4	224	17	T47158	yB53a08.s1 Homo sapie 6.59e-11
40	29	0.4	269	87	H63862	yu47d11.s1 Homo sapie 6.59e-11
c 41	29	0.4	336	161	AA052285	mb15a01.r1 Soares mou 6.59e-11
c 42	29	0.4	382	117	W33907	mc56g04.r1 Soares mou 6.59e-11
c 43	29	0.4	407	110	HUM161B09B	Human fetal brain cDN 6.59e-11
c 44	29	0.4	498	34	R81313	yJ01g06.r1 Homo sapie 6.59e-11
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ALIGNMENTS

RESULT 1
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DEFINITION H. sapiens partial cDNA sequence; clone c-2hd06.
ACCESSION F07776
NID 9677276
KEYWORDS partial cDNA sequence; transcribed sequence fragment.
SOURCE human.

Tue Oct 14 14:18:11 1997

ORGANISM	Homio sapiens
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata: Vertebrata: Eutheria; Primates: Catarrhini; Hominidae; Homo. 1 (bases 1 to 343)
AUTHORS	Genexpress.
TITLE	Direct Submission
JOURNAL	Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Molculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr
REFERENCE	2 (bases 1 to 343)
AUTHORS	Genexpress.
TITLE	The Genexpress cDNA program
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 343)
AUTHORS	Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houliatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Marriage-Samson,R., Pietu,G., Pouliot,Y., Sebatiani,Kabatchis,C. and Tessier,A.
TITLE	IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE	95277534
COMMENT	Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lacmid BA vector; Sequencing_method: single read, full automatic; Primer: M13 reverse cDNA sequence colinear to mRNA Stretch_removed: nothing Normalization_method: Bento Soares, P.N.A.S. 91:9228-9232(1994); Genexpress_library_id: C; Genexpress_sequence_id: Ylc-2hd06. Genexpress_location/Qualifiers 1..343 /organism="Homo sapiens" /isolate="muscular atrophy patient" /clone_lib="normalized infant brain cDNA from B.Souares, Psychiatry Dept. Columbia University USA" /sex="female" /tissue="total brain" /dev_stage="3 months old" /dev_stage="80 g 112 t 5 others BASE COUNT 68 a 78 c 80 g 112 t 5 others ORIGIN Query Match 1.9%; Score 124; DB 107; Length 343; Best Local Similarity 67.3%; Pred. No. 5.78e-208; Matches 231; Conservative 0; Mismatches 112; Indels 0; Gaps 0; Db 1 ttctctccattgtaggaatttcttgcctgaactgataagaaatatttctgtgcctca 60 Qy 5140 TTTTATCCATCTTAGGCTTGTACTTAGCGATATATCGAGAGTACTTGTGTCGCCGA 5199 Db 61 cctgttgcagatgcctgttcgagattgcccgaactcactcgtctgatacaaggag 120 Qy 5200 CCGTGTCCGAGTGGTGGCGTGGGGAAGTGGCGCGGTCTCTTCGACTGGTGAAGGGAG 5259 Db 121 caaaggggacccgcagcgtctcttctgttgatgatctccctccgtctgtttaaca 180 Qy 5260 CCAAGGGCATTCGGACACTGCTTCGCGGTGGCCATCTGCTGCGGCCCTGTCAACA 5319 Db 181 tcggnctcctcttccctccggatcttcatctacncaatcttgggagatgccaatattg 240 Qy 5320 TCTGCCCTGCTGCTTCCCTGGTCATGTTTCATCTTTGCCATTTTCGGCATGTGCTCTCA 5379 Db 241 cctatgttaagagggaagtggatcgatgacatgttannctttagacccttggcaaca 300 Qy 5380 TGCACGTGAAGGAGAAGAGCGGATTAACGACGCTACAACTTCAGACCTTTGCCAGA 5439 Db 301 gcatgatctcctgttccaaattacaacctctgctggctggga 343 Qy 5440 GCATGATCTCCTCTTTTCAGATGTCGACGTCACCGCGTGGGA 5482

[illegible]

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/lab_host="SOLR (kanamycin resistant)"
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RESULT 15
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DEFINITION Human clone xs430 mRNA sequence.
ACCESSION U46419
NID g1245087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 389)
AUTHORS Mueller-Pillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-1996) Internal Medicine I, University of Ulm,
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany
FEATURES
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/tissue_type="pancreatic cancer"
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Search completed: Sat Oct 11 04:38:40 1997
Job time : 4112 secs.

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W P E R E L E H

(TM)

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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Oct 11 04:39:02 1997; MasPar time 1701.24 seconds
Tabular output not generated. 1052.078 Million cell updates/sec

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Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTAGAGTTGGCGGCATAG.....ACGGAGTATAGTCTAGA 6513
Comp: AGATCTGCAACCGCGGTATC.....TGCCTCATATCGAGATCT

Scoring table:
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 359085 seqs, 137405154 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS-THREE
1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204
7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210
13:EST211 14:EST212 15:EST213 16:EST214 17:EST215
18:EST216 19:EST217 20:EST218 21:EST219 22:EST220
23:EST221 24:EST222 25:EST223 26:EST224 27:EST225
28:EST226 29:EST227 30:EST228 31:EST229 32:EST230
33:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3
39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
46:STS11 47:STS12 48:STS13
EST-STS-FOUR
49:gnEST1 50:gnEST2 51:gnEST3 52:gnEST4 53:gnEST5
54:gnEST6 55:gnEST7 56:gnEST8 57:gnEST9 58:gnEST10
59:gnEST11 60:gnEST12 61:gnEST13 62:gnEST14 63:gnEST15
64:gnEST16 65:gnEST17 66:gnEST18 67:gnEST19 68:gnEST20
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99:enEST25 100:enEST26 101:enEST27 102:enEST28
103:enEST29 104:enEST30 105:enEST31 106:enSTS 107:ueEST1
108:ueEST2

Database:

EST-STS-FOUR

Statistics: Mean 12.744; Variance 2.217; scale 5.749
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result % Query

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description	Pred. No.
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3	43	0.7	225	23	AA214661	zq89e09.r1 Stratagene	1.99e-33
4	31	0.5	179	73	HSU46448	Human EST overexpress	1.16e-13
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8	34	0.5	271	41	G16013	human STS CHLC.GCT13C	3.48e-12
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10	32	0.5	289	39	G09716	human STS CHLC.GCT10F	3.59e-15
11	32	0.5	323	105	MMW4171	mf85a01.r1 Soares mou	3.59e-15
12	32	0.5	337	36	DM3441T	D. melanogaster STS d	3.59e-15
13	32	0.5	352	56	AA145456	mr10b01.r1 Soares mou	3.59e-15
14	32	0.5	356	52	AA168767	ms36h04.r1 Stratagene	3.59e-15
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19	30	0.5	403	48	PCU64654	Parachartergus colobo	3.48e-12
20	31	0.5	408	47	HUME1100	Human genomic DNA, se	1.16e-13
21	31	0.5	408	46	HUME1100	Human genomic DNA, se	1.16e-13
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25	32	0.5	442	21	AA022705	zr71c03.s1 Soares pre	3.59e-15
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42	30	0.5	606	41	G16005	human STS CHLC.GCT10H	3.48e-12
43	31	0.5	696	48	PRU64637	Pollistes bellicosus m	1.16e-13
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ALIGNMENTS

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LOCUS ms53e02.r1 Life Tech mRNA EST 07-JAN-1997
DEFINITION cDNA clone 615290 5', similar to gb:M81758 SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); gb:U26707 Mus musculus voltage-gated sodium channel alpha subunit SCN8A (MOUSE);;
ACCESSION AL183990
NID G1767357
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 529)
AUTHORS Maria.M., Hillier.L., Allen.M., Bowles.M., Dietrich.N., Dubuque.T., Geisel.S., Kucaba.T., Lacy.M., Le.M., Martin.J., Morris.M., Schellenberg.K., Steptoe.M., Tan.F., Underwood.K., Moore.B., Theising.B., Wylie.T., Lennon.G., Soares.B., Wilson.K. and Waterston.R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)

US-08-554-424-7.1st2

Tue Oct 14 14:18:12 1997

COMMENT

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:376114
Seq primer: -28M13 revl from Amersham
High quality sequence stop: 263.

FEATURES

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RESULT 2 standard; RNA; EST; 529 BP.

ID MAA83990
AC AA183990;
NI 91767357
DT 21-FEB-1997 (Rel. 51, Created)
DE ms35e02 r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus
DE CDNA clone 615290 5', similar to gb:M81758 SODIUM CHANNEL PROTEIN,
DE SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); gb:U26707 Mus musculus
DE voltage-gated sodium channel alpha subunit SCN8A (MOUSE).
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]

1-529
RP Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wyllie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.,
RA "The WashU-HHMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LLNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:376114 Seq
CC primer: -28M13 revl from Amersham High quality sequence stop: 263.
FH Location/Qualifiers
Key
FT source
FT 1..529
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FT PCMV-SPORT2 vector."
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Best Local Similarity 70.1%; Pred. No. 8.43e-196;
Matches 220; Conservative 0; Mismatches 93; Indels 1; Gaps 1;
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QY 5493 GACGCCATTATCAA 5506
RESULT 3
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DEFINITION zq89e09.r1 Stragene hnt neuron (#937233) Homo sapiens CDNA clone
649192 5', similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II
ALPHA SUBUNIT (HUMAN).
ACCESSION AA214661
NID g1813315
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 225)

denature:	30 seconds at 94 degrees C
annealing:	75 seconds at 55 degrees C
extension:	15 seconds at 72 degrees C

TITLE	COMMENT
Waterston, R. The WashU-HHMI Mouse EST Project Unpublished (1996)	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800

Email: mousestewatson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:374511
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 279.
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 /strain="NIH/Swiss"
 FEATURES
 source

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364 bp							
DNA							
STS							
19-OCT-1995							

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 364)
Hudson.T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped STS
Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu
 Primer A: CCCACTCCATGGATGAAGAA
 Primer B: AACTACTGGCACAAAGTATTC
 STS size: 275

Search completed: Sat Oct 11 05:13:35 1997
Job time : 2073 secs.